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(54) Title: **POLYPEPTIDES FOR IDENTIFYING NEW HERBICIDALLY ACTIVE COMPOUNDS**

(57) Abstract: The invention relates to a method of identifying plant-specific polypeptides and nucleic acids encoding them which are suitable as sites of action for finding herbicides, to the use of the polypeptides identified for identifying new, herbicidally active compounds, and methods of finding modulators of these polypeptides. Likewise, the invention relates to the use of the polypeptides in assay methods for identifying herbicidally active compounds.

Polypeptides for identifying new herbicidally active compounds

The invention relates to a method of identifying plant-specific polypeptides and nucleic acids encoding them which are suitable as sites of action for finding
5 herbicides, to the use of the polypeptides which have been identified for identifying new herbicidally active compounds, and to methods of finding modulators of this polypeptide. Equally, the invention relates to the use of the plant polypeptides in assay methods for identifying herbicidally active compounds.

10 Herbicides have great importance in agriculture to avoid undesired plant growth by using herbicides. In modern agriculture, the use of herbicides constitutes an imperative factor for safeguarding yields and profits. This is where herbicides must meet increasingly high demands with regard to their efficacy, costs and above all their ecofriendliness. There is therefore a constant demand for new substances,
15 known as lead structures, which can be developed into even more potent and even more ecofriendly new herbicides.

To date, only a few molecular sites of action, known as targets, play a key role for the action of herbicidal compounds. Three quarters of the entire herbicide market are
20 dominated by just 5 targets, which are the sites of action of these herbicides: acetolactate synthase, elongases for very long-chain fatty acids, enolpyruvylshikimate-3-phosphate synthase, the photosystem II and the auxin signal cascade. The remaining quarter of the market comprises just 6 further important targets: acetal-coenzyme A carboxylase, glutamine synthase, photosystem I, phytoene
25 desaturase, protoporphyrinogen oxidase and tubulin. Herbicides for all of these targets have been known for over 20 years. During this period, herbicides with other, new targets have not gained market relevance. This situation leads to a thorough knowledge and exploitation of these targets in the search for new herbicidally active lead structures. At the same time, however, the use of new targets is extremely
30 important for an innovation in the search for new lead structures for the development of novel and superior herbicides.

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To date it is generally customary to search for new lead structures in greenhouse tests. However, such tests require a good deal of labour and are expensive. The number of the substances, which can be tested in the greenhouse, is accordingly limited. However, even after suitable automation for increasing the throughput, greenhouse screening does not allow any findings as to whether substances may be directed against a new target. This must be determined in very complex subsequent experiments.

10 An alternative to the search for lead structures which is nowadays generally customary is what is known as high-throughput screening or ultra-high-throughput screening (HTS or UHTS). This method, which was first established in pharmaceutical research, makes possible the automation of in-vitro assays for the search for lead structures for given targets. At the same time, it has been made possible to provide a high number of test substances by methods such as, for example, combinatorial chemistry. Thus, a multiplicity of methods has been developed as to how specific targets can be assayed by (U)HTS. The target-based search for lead structures for agricultural applications with the aid of (U)HTS does not differ from that for pharmaceutical applications and is therefore firmly established at present.

(U)HTS makes it possible to test the action of several hundreds of thousands of substances on a specific target within a few days. However, existing experience in industry shows that it is not possible to find a lead structure for each new target, at least not at present. It is therefore necessary to test a multiplicity of targets in order to identify suitable targets in addition to new herbicidal substances.

All of the five abovementioned herbicide targets which dominate the market, and most of the remaining targets, are only found in plants but not in animals. This is no coincidence but is due to the advantageous properties of such active compounds. Thus, there is only little danger of a toxic effect on humans and the environment in

plant-specific targets. This can be proved by comparing the two targets acetolactate synthase and protoporphyrinogen oxidase. At the beginning of the 80s, highly effective and innovative compounds were discovered for both targets, initially without knowing the target. A series of herbicides were quick to reach the market in the case of the plant-specific target acetolactate synthase, so that acetolactate synthase is currently ranked third among the herbicide targets. Even though a very large variety of herbicides which act on protoporphyrinogen oxidase, which is also found in animals, is now known, the unfavourable toxicology of these products has as yet not led to an important commercial product.

Toxicological studies are complicated and expensive. As a rule, these studies are only performed when a certain basic development of new lead structures has already taken place. Even so, the research expenses up to this point are quite considerable. It is therefore advantageous to minimize the toxic effect of new herbicides, which is due to the target, right at the beginning. This can be achieved by simply using those targets for the search for lead structures which are found only in plants, but not in animals.

Especially advantageous targets for new herbicides are searched for in essential biosynthetic pathways. Thus, for example, the biosynthesis of isoprenoids, building blocks of carotenoids and of plastoquinone and chlorophyll, are imperative for the growth of plants. The inhibition of a step in this plant-specific biosynthetic pathway, also known as the 1-desoxyxylulose-5-phosphate pathway, leads to the death of a plant (DE 199 35 967). The knowledge of the plant specificity of specific metabolic pathways is currently fundamental knowledge in plant biochemistry (see, for example, B. B. Buchanan, W. Gruissem and R. L. Jones (Editors); "Biochemistry & Molecular Biology of Plants", American Society of Plant Physiologists, Rockville, MD, USA; 2000), even when it remains partially unclear which role certain proteins take on in the plant, and whether corresponding proteins or those with an equivalent task are also found in, for example, mammals.

Each new candidate herbicide must meet a number of criteria before it can be approved, and the choice of a suitable target is the first step in this search.

5 It is helpful to consider the existing genome information which is now available to the public, and to take note of some key criteria of herbicidal active compounds:

1. An active compound should be sufficiently selective and produce a herbicide which should be specific, or at least very selective, for plants (with regard to humans or animals).
- 10 2. An active compound should attack proteins or else genes which are imperative for the growth or the viability of the undesired plants, and
- 15 3. something should be known about the function of the target protein or target gene so that an assay and high-throughput screens can be established.

It is furthermore important for choosing suitable targets that the probability of identifying a new lead structure is considerably higher when the target has a natural binding property for ligands of low molecular weight. This is in contrast to, for example, individual protein components of large complexes with many subunits. The interference of protein-protein interactions by small ligands is less possible and requires, in principle, larger active compounds whose production costs are then frequently higher, so that a meaningful use of these active compounds as herbicides is made substantially more difficult. Targets with small natural ligands are, for example, enzymes, receptors and channels. Moreover, enzymes, receptors and channels can frequently be assayed more easily in assay methods (HTS or UHTS) than other proteins.

30 A possibility of recognizing plant-specific new targets is to test the enzymes or receptors and channels involved in plant-specific metabolic pathways or signal chains one after the other, using present-day biochemical knowledge (B. B. Buchanan, W.

Gruissem and R. L. Jones (Editors); "Biochemistry & Molecular Biology of Plants", American Society of Plant Physiologists, Rockville, MD, USA; 2000). However, this route carries the risk of overlooking important properties of the proteins.

5 While new routes for, for example, based on sequence information in the field of antibiotic research have already been described (see, for example, Molly B. Schmid, Novel approaches to the discovery of antimicrobial agents, Curr. Opin. Chemical Biol., 2, 529-534, 1998.), a method of identifying suitable targets for the search for herbicides on the basis of existing data from sequencing work is as yet not available.

10

It was therefore the object of the present invention to describe a method which is suitable for identifying, in an efficient and reliable fashion, those nucleic acids or polypeptides encoded by them from among sequence information available in public databases, which can be used for the search for new herbicidal active compounds as plant-specific sites of action which can be obtained by a screening method. The object of the present invention was also to identify and to describe suitable target proteins by means of the method described and to make these available for use in screening methods for the search for new active compounds.

15

20 The complete knowledge of the genome of *Arabidopsis*, of humans and of many other organisms now allows to filter out, by means of computer-aided comparison of the proteins encoded in the genome, those proteins which occur in one organism but not another. Thus, it is also possible to recognize plant-specific proteins whose function was hitherto unelucidated.

25

In the present context, the term "plant-specific" is understood as meaning that no similarity with proteins from animals, in particular higher animals (Metazoa; in particular Chordata) is found.

30

A series of these plant-specific proteins, however, are also found in micro-organisms (for example bacteria, fungi).

In the present invention there is now described a possibility of identifying, from publicly available information and with the aid of computer-aided methods, those proteins and the nucleic acids encoding them which are suitable for use in methods for identifying new herbicidally active compounds.

The comparison of the proteins encoded in various genomes is possible by means of a systematic alignment comparison (for example BLAST (Altschul et al., 1990), FastA (Lipman and Pearson, 1985, Pearson 1991), Search (Smith and Waterman, 1981) Hmmer (Durbin et al., 1998)) between all proteins of one organism and those of the other organism. Preferably, one organism is selected, and the presence of the homologous sequence in other organisms is then studied.

In the present invention, all of the proteins encoded in the genome of *Arabidopsis thaliana* (hereinbelow abbreviated to "Arabidopsis") are compared with all of the other sequences which are accessible in public databases. The following databases were used as source for the Arabidopsis polypeptides in the present invention:

- a) TAIR (Huala et al., 2001), which is a searchable relational database comprising information related to *Arabidopsis thaliana*, and
- b) GenBank (Benson et al., 2000), which is the NIH genetic sequence database, an annotated collection of all publicly available DNA sequences, including protein translations.

Databases which can be used for the comparison are, for example, the following:

- a) SwissProt, which is a curated protein sequence database and provides a high level of annotations (e.g. function, domains structure, variants etc.)
- b) TrEMBL and TrEMBL-New (non-redundant protein databases), which are computer-annotated supplements of Swiss Prot and contain all the translations of EMBL nucleotide sequence entries not yet integrated in SwissProt and

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whereby TrEMBL-New is a weekly update to TrEMBL which contains the protein-coding sequences from EMBLNEW

(see Bairoch and Apweiler, 2000).

5

All of the protein-encoding genes, and/or the polypeptides encoded by them, of the databases are compared with each other (pair-wise comparison; each polypeptide with each polypeptide) in order to find homologous similarities. The rigorous Smith-Waterman algorithm is used for this purpose.

10

To assess whether a given alignment constitutes evidence for homology, it helps to know how strong an alignment can be expected from chance alone. A local alignment without gaps consists simply of a pair of equal length segments, one from each of the two sequences being compared. A modification of the Smith-Waterman or Sellers algorithms will find all segment pairs whose "scores" can not be improved by extension or trimming. These are called high-scoring segment pairs (HSPs). To analyze how high a score is likely to arise by chance, a model of random sequences is needed. For proteins, the simplest model chooses the amino acid residues in a sequence independently, with specific background probabilities for the various residues. In the limit of sufficiently large sequence lengths m and n , the statistics of HSP scores are characterized by two parameters, K and λ . Most simply, the expected number of HSPs with score at least S is given by the formula

15

20

$$E = Kmne^{-\lambda S}$$

25

which is the so called E-value for the score S . The parameters K and λ can be thought of simply as natural scales for the search space size and the scoring system respectively.

30

The measure for the similarity which is obtained is therefore an E-value (expect-value). As shown above, the E-value indicates the probability of which the existing

agreement between two proteins or else genes or nucleic acids is due to pure random chance. The smaller the E-value, the more significant a hit in the search. If, for example, the E-values are in the range of $1e-70$, this means that owing to the size of the database, only 10^{-70} hits would have been expected with the search sequence.

5 This also means that the results are highly significant. In the case of two identical sequences, the E-value thus progresses towards zero. In the case of two entirely unrelated sequences, the E-value converges to values greater than one.

In the present method according to the invention, the criterion chosen for plant

10 specificity and thus the suitability of the polypeptide according to the present invention, the E-value was chosen such that the exponent of the E-value of a paralogous or orthologous plant amino acid sequence must exceed that of a corresponding paralogous or orthologous animal or human sequence, in as far as such an animal or human sequence exists, at least by a factor of 3. The E-value of 10^{-30} is

15 particularly suitable as limit for defining plant specificity. If the abovementioned factor decreases, it can be assumed with high probability that the homology between the plant sequence and the animal or human sequence is too high to classify a plant polypeptide as plant-specific and suitable for the use according to the invention in methods of finding herbicides.

20 The term "identity" as used in the present context refers to the number of sequence positions which are identical in an alignment. In most cases, it is indicated as a percentage of the alignment length.

25 The term "similarity" as used in the present context, in contrast, requires the definition of a similarity matrix, that is to say a measure for the degree of similarity one wishes to assume between, for example, a valine and a threonine or a leucine.

The term "homology" as used in the present context, in turn, refers to evolutionary

30 relationship. Two homologous proteins have developed from a joint precursor sequence. The term does not necessarily imply identity or similarity, apart from the

fact that homologous sequences are usually more similar (or have more identical positions in an alignment) than non-homologous sequences.

The term "orthologues" or "orthologous" as used in the present contexts refers to a functional counterpart, for example a protein in another organism, both having developed from a shared precursor. Normally, orthologues retain a shared function. In contrast, "paralogues" are genes or proteins resulting therefrom which have originated by duplication within a genome and which have assumed different functions during evolution which may still have similarity with each other.

Proteins are termed orthologous when

1. they have the highest level of pair-wise similarity (compared with the identities of the two proteins with all the other proteins in other genomes) and
2. the similarity is significant ($E < 0.01$).

The proteins encoded in the *Arabidopsis* genome and the results of the comparison with all the other public sequences were stored in a relational database (Oracle) in the present invention.

Such a relational database model was presented in 1970 by Codd et al. All of the data to be processed are shown in Tables (relatins) with a fixed number of columns and any desired number of lines (tupels). Data redundancies are avoided by distributing the information to individual tables. To date, this model remains the basis of most of the commercial database systems.

In general, the assigning of a description which is firstly correct and can secondly be searched for readily, what is known as an annotation, to each sequence constitutes a major problem in practice. An "annotation" of a sequence is the assigning of biologically relevant properties to this sequence of parts thereof.

By comparison of, possibly competing, alternative annotations in public databases and by individual corrections, a standardized annotation for each database entry has now been generated in the present invention. For example, the annotation takes such
5 a form that the description of enzymes, receptors and channels (transporters) starts with the respective functional name, that is, for example, with "acetolactate synthase".

10 An annotation was assigned to the sequence in a multi-step process: first, the information content of words or terms within a sequence description were analysed and these words/terms were correspond categorized. Thus, the description "acetolactate synthase" leads to more information on a sequence than the descriptions "Unknown Protein" or "Hypothetical Protein" or "exon predicted by xgrail, quality marginal_shadowexon". This procedure first gives two categories of words/terms
15 and, based on these categories, eventually two categories or sequence descriptions: those with a low information content and those with a high information content.

Only the sequence descriptions with a high information content are used for assigning an annotation to a sequence. These annotations obtained in this way are
20 subsequently aligned in a suitable fashion with the annotations obtainable from TAIR. In the present invention, the TAIR annotation for a given sequence was adopted if such an annotation did exist.

This process was automated by developing suitable programs .
25

In a final step, the present annotations were rechecked and, if appropriate, corrected, to arrive at the final standardized annotation.

30 The database established within the present invention contains sequences from Arabidopsis and the relevant descriptions(annotations) and E values in question and thus makes possible an efficient and meaningful analysis of the sequence data, which

results in the reliable identification of suitable plant-specific targets for the purposes of the present invention.

5 All the enzymes, receptors and channels or transporters with the above-described plant-specific E-values were then filtered out from the annotations of the database according to the invention with the aid of a suitable algorithm with suitable search terms. The polypeptides found by this method are shown in Table 1. In addition to the annotation of the polypeptide whose sequence is available by means of the reference to the sequence listing in the present application, Table 1 also shows which
10 particular class of polypeptides it belongs to. Enzymes were arranged for example by classes such as "dehydrogenase" or "oxygenase". Receptors were searched for with the search term "receptor", but not "receptor kinase". Channels were searched for with the search term "channel" or "transporter". The table also contains what is known as the accession number of the sequence, in as far as it is known. The
15 accession number provides information on the database or the number in which, or under which, the polypeptide sequence in question can be found. Furthermore, the table contains references to known homologous sequences from other organisms and a reference to the SEQ ID NO. under which the sequence in question is filed in the sequence listing.

20

Table 1:

| ENTRY ID NO. | SEQ ID NO. | DESCRIPTION | CLASS |
|-----------------|---------------|---|-----------------|
| 5 | 1 | INORGANIC PYROPHOSPHATASE, PUTATIVE SIMILAR TO SOLUBLE INORGANIC PYROPHOSPHATASE GB: AAD46520 GI:5669924 FROM [POPULUS TREMULA X POPULUS TREMULOIDES] | Phosphatase |
| 12 | 2 | FATTY ACID ELONGASE 3-KETOACYL-COA SYNTHASE 1 IDENTICAL TO GB:AAC99312 GI:4091810 FROM [ARABIDOPSIS THALIANA] | Synthase |
| 33 | 3 | CYCLIC NUCLEOTIDE AND CALMODULIN-REGULATED ION CHANNEL, PUTATIVE SIMILAR TO CYCLIC NUCLEOTIDE AND CALMODULIN-REGULATED ION CHANNEL GB:CAB40128 GI:4581201 FROM [ARABIDOPSIS THALIANA] | Channel |
| 38 | 4 | FLAVONOL 3-O-GLUCOSYLTRANSFERASE, PUTATIVE SIMILAR TO FLAVONOL 3-O-GLUCOSYLTRANSFERASE GB:Q40287 FROM [MANIHOT ESCULENTA] | Transferases |
| 41 | 5 | FLAVONOL 3-O-GLUCOSYLTRANSFERASE, PUTATIVE SIMILAR TO FLAVONOL 3-O-GLUCOSYLTRANSFERASE GB:Q40287 FROM [MANIHOT ESCULENTA] | Transferases |
| 46 | 6 | 1-PHOSPHATIDYLINOSITOL-4-PHOSPHATE KINASE(ATPIP5K1) GI:3702691 FROM [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN CONTAINS SIMILARITY TO] | 5-Kinase |
| 50 | 7 | DEHYDROGENASE GI:1922246 FROM [ARABIDOPSIS THALIANA] UNKNOWN PROTEIN SIMILAR TO PUTATIVE | Dehydrogenases |
| 53 | 8 | SERINE/THREONINE KINASE, PUTATIVE SIMILAR TO SERINE/THREONINE KINASE GI:7248457 FROM [LOPHOPYRUM ELONGATUM] | Kinase, Protein |
| 57 | 9 | FERRIC REDUCTASE LIKE TRANSMEMBRANE COMPONENT | Reductase |
| 58 | 10 | FERRIC REDUCTASE LIKE TRANSMEMBRANE COMPONENT | Reductase |

| | | | |
|-----|----|--|-----------------|
| 72 | 11 | PROTEIN KINASE, PUTATIVE SIMILAR TO PROTEIN KINASE GB:BAA24694 GI:2852447 FROM [ARABIDOPSIS THALIANA] | Kinase, Protein |
| 77 | 12 | K EFFLUX ANTIporter KEA1 IDENTICAL TO GB:AAD01191 GI:4101473 FROM [ARABIDOPSIS THALIANA] | Transporter |
| 83 | 13 | DIMETHYLADENOSINE TRANSFERASE, PUTATIVE, 5' PARTIAL SIMILAR TO DIMETHYLADENOSINE TRANSFERASE GB:AAC09322 GI:3005590 FROM [ARABIDOPSIS THALIANA] | Transferases |
| 85 | 14 | CUCUMISIN-LIKE SERINE PROTEASE GB:AAC18851 GI:317687 FROM [ARABIDOPSIS THALIANA]4[HYPOTHETICAL PROTEIN CONTAINS SIMILARITY TO] | Protease |
| 87 | 15 | RIBULOSE-1,5 BISPHTHOSPHATE CARBOXYLASE GB:L34291 GI:508550 FROM [PISUM SATIVUM][HYPOTHETICAL PROTEIN CONTAINS SIMILARITY TO] | Carboxylase |
| 93 | 16 | RETICULINE OXIDASE-LIKE PROTEIN GB:CAB45849 GI:5262223 FROM [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN SIMILAR TO] | Oxidase |
| 95 | 17 | NUCLEOTIDE SUGAR EPIMERASE, PUTATIVE SIMILAR TO NUCLEOTIDE SUGAR EPIMERASE GB:AAC18831 GI:3093975 FROM [VIBRIO VULNIFICUS] | Epimerase |
| 100 | 18 | CHALCONE SYNTHASE HOMOLOG, GP U90341 2507617 AND ANOTHER SPECIFIC PROTEIN, GP Y14507 2326772 | Synthase |
| 118 | 19 | SER-THR PROTEIN KINASE-LIKE PROTEIN GI:9294588 FROM [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN SIMILAR TO] | Kinase, Protein |
| 127 | 20 | (1-4)-BETA-MANNAN ENDOHYDROLASE PRECURSOR, PUTATIVE SIMILAR TO (1-4)-BETA-MANNAN ENDOHYDROLASE PRECURSOR GI:9836826 FROM [LYCOPERSICON ESCULENTUM] | Hydrolase |
| 132 | 21 | CHITINASE, PUTATIVE SIMILAR TO CHITINASE GI:1237025 FROM [ARACHIS HYPOGAEA] | Chitinase |
| 136 | 22 | DIOXYGENASE, PUTATIVE SIMILAR TO DIOXYGENASE GI:1666096 FROM [MARAH MACROCARPUS] | Oxygenases |

| | | | |
|-----|----|--|--------------|
| 142 | 23 | POLYGALACTURONASE PG1, PUTATIVE SIMILAR TO POLYGALACTURONASE PG1 GB:AAD46483 GI:5669846 FROM [GLYCINE MAX]. | Glycosylase |
| 154 | 24 | ALDEHYDE OXIDASE, PUTATIVE SIMILAR TO ALDEHYDE OXIDASE GB:BAA28630 GI:3172044 FROM [ARABIDOPSIS THALIANA] | |
| 157 | 25 | NUCLEOSIDE TRANSPORTER GB:AAF26446 GI:6715514 FROM [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN SIMILAR TO][PUTATIVE] | Transporter |
| 158 | 26 | BETA-XYLOSIDASE, PUTATIVE SIMILAR TO BETA-XYLOSIDASE GB:Z84377 GI:2102655 FROM [ASPERGILLUS NIGER] | Glycosylase |
| 166 | 27 | GLYCOSYL TRANSFERASE GB:CAB80706 GI:7268597 FROM [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN SIMILAR TO][PUTATIVE] | Transferases |
| 167 | 28 | CELLULOSE SYNTHASE CATALYTIC SUBUNIT GB:AAC39336 GI:2827143 FROM [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN SIMILAR TO] | Synthase |
| 172 | 29 | POLYGALACTURONASE, PUTATIVE SIMILAR TO POLYGALACTURONASE GI:288611 FROM [ZEA MAYS] | Glycosylase |
| 174 | 30 | PECTINESTERASE, PUTATIVE SIMILAR TO PECTIN ESTERASE GI:1213628 FROM [PRUNUS PERSICA] | Esterase |
| 185 | 31 | GLUTATHIONE S-TRANSFERASE, PUTATIVE SIMILAR TO GLUTATHIONE S-TRANSFERASE GI:860955 FROM [HYOSCYAMUS MUTICUS] | Transferases |
| 186 | 32 | GLUTATHIONE S-TRANSFERASE, PUTATIVE SIMILAR TO GLUTATHIONE S-TRANSFERASE GI:860955 FROM [HYOSCYAMUS MUTICUS] | Transferases |
| 187 | 33 | GLUTATHIONE S-TRANSFERASE, PUTATIVE SIMILAR TO GLUTATHIONE S-TRANSFERASE GI:860955 FROM [HYOSCYAMUS MUTICUS] | Transferases |
| 188 | 34 | GLUTATHIONE-S-TRANSFERASE, PUTATIVE SIMILAR TO GLUTATHIONE-S-TRANSFERASE GI:169887 FROM [SILENE VULGARIS] | Transferases |

| | | | |
|-----|----|---|----------------|
| 197 | 35 | LIPOAMIDE DEHYDROGENASE COMPONENT OF THE PYRUVATE DEHYDROGENASE COMPLEX E3, CONTAINS PF 00010 HELIX-LOOP-HELIX DNA-BINDING DOMAIN. ESTS GB T45640 AND GB T22783 COME FROM THIS GENE[PUTATIVE] | Dehydrogenases |
| 209 | 36 | FRUCTOKINASE, PUTATIVE PREDICTED BY GENEFINDER | Kinase |
| 224 | 37 | ISOAMYLASE SIMILAR TO GI 1652733 GLYCOGEN OPERON PROTEIN GLGX FROM SYNECHOCYSTIS SP. GENOME GB D90908. ESTS GB H36690, GB AA712462, GB AA651230 AND GB N95932 COME FROM THIS GENE[PUTATIVE] | Glycosylase |
| 232 | 38 | ANTHRANILATE HYDROXYCINNAMOYL/BENZOYLTRANSFERASE[HYPOTHETICAL PROTEIN SIMILAR TO] | N-Transferases |
| 233 | 39 | 1-AMINOCYCLOPROPANE-1-CARBOXYLATE OXIDASE SIMILAR TO ESTS EMB Z34690, GB T04168, GB H37738, GB T76913, GB T43801, AND GB T21964[PUTATIVE] | Oxidase |
| 234 | 40 | 1-AMINOCYCLOPROPANE-1-CARBOXYLATE OXIDASE SIMILAR TO ESTS EMB Z34690, GB T04168, GB H37738, GB T76913, GB T43801, AND GB T21964[PUTATIVE] | Oxidase |
| 243 | 41 | ANTHOCYANIN 5-AROMATIC ACYLTRANSFERASE GB:BAA74428[HYPOTHETICAL PROTEIN SIMILAR TO] | Transferases |
| 250 | 42 | PROTEIN PHOSPHATASE SIMILAR TO GB:AAB97706[PUTATIVE] | Phosphatase |
| 254 | 43 | PROTOCHLOROPHYLLIDE REDUCTASE SIMILAR TO PROTOCHLOROPHYLLIDE REDUCTASE PRECURSOR; SIMILAR TO ESTS GB R30630, GB T46162, EMB Z26728, GB AA042736, AND GB AA042730[PUTATIVE] | Reductase |
| 284 | 44 | ANTHOCYANIN 5-AROMATIC ACYLTRANSFERASES[HYPOTHETICAL PROTEIN NEARLY IDENTICAL TO], ARABIDOPSIS PROTEIN F21B7.22, SIMILAR TO | Transferases |
| 294 | 45 | ACID PHOSPHATASE; LOCATION OF ESTS 110C2T7, GB T42036, AND 110C2XP, GB AI100245; SIMILAR TO | Phosphatase |

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| 297 | 46 | MITOCHONDRIAL IMPORT RECEPTOR SUBUNIT HYPOTHETICAL GB Z98597 FROM S. POMBE. ESTS GB T45575 AND GB Z26435 AND GB AA394576 COME FROM THIS GENE | Receptor |
| 301 | 47 | SUBTILISIN PROTEASE STRONG SIMILARITY TO PROTEIN SBT1 GB X98929 FROM LYCOPERSICUM ESCULENTUM[PUTATIVE] | Protease |
| 302 | 48 | ABC TRANSPORTER, MULTI-DRUG RESISTANCE PROTEIN STRONG SIMILARITY TO MRP-LIKE ABC TRANSPORTER GB U92650 FROM A. THALIANA AND CANALICULAR MULTI-DRUG RESISTANCE PROTEIN GB L49379 FROM RATTUS NORVEGICUS | Transporter |
| 303 | 49 | SERINE/THREONINE PROTEIN PHOSPHATASE GB X83099 FROM S. CEREVISIAE[HYPOTHETICAL PROTEIN CONTAINS SIMILARITY TO] | Phosphatase |
| 305 | 50 | PHOSPHORIBOSYLANTHRANILATE TRANSFERASE [PUTATIVE] | Transferases |
| 308 | 51 | DIMETHYLANILINE MONOOXYGENASE [PUTATIVE] | Oxygenases |
| 311 | 52 | ADENYLATE CYCLASE GB AF012921 FROM MAGNAPORTHE GRISAE. EST GB Z24512 COMES FROM THIS GENE; UNKNOWN PROTEIN CONTAINS SIMILARITY TO | Cyclase |
| 312 | 53 | BETA-KETOACYL-COA SYNTHASE STRONG SIMILARITY TO BETA-KETO-COA SYNTHASE GB U37088 FROM SIMMONDSIA CHINENSIS[PUTATIVE] | Synthase |
| 321 | 54 | ETHYLENE RECEPTOR (ERS2) EST GB W43451 COMES FROM THIS GENE[PUTATIVE] | Receptor |
| 324 | 55 | 1-AMINOCYCLOPROPANE-1-CARBOXYLATE OXIDASE SIMILAR TO ARABIDOPSIS 2A6 (GB X83096). EST GB T76913 COMES FROM THIS GENE[PUTATIVE] | Oxidase |
| 327 | 56 | 1-AMINOCYCLOPROPANE-1-CARBOXYLATE OXIDASE STRONG SIMILARITY TO ARABIDOPSIS 2A6 (GB X83096)[PUTATIVE] | Oxidase |
| 331 | 57 | ALDO-KETO REDUCTASE BABESIA (GB M93122[HYPOTHETICAL PROTEIN SIMILAR TO]) | Reductase |

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| 350 | 58 | DIMETHYLANILINE MONOOXYGENASE SIMILAR TO GB:AAC04900[PUTATIVE] | Oxygenases |
| 357 | 59 | PECTATE LYASE A11 SIMILAR TO GB:CAB36835[PUTATIVE] | Lyase |
| 380 | 60 | SUCROSE-PHOSPHATE SYNTHASE, PUTATIVE SIMILAR TO GB:Y11795 FROM [CRATEROSTIGMA PLANTAGINEUM] | Synthase |
| 390 | 61 | 1-AMINOCYCLOPROPANE-1-CARBOXYLATE OXIDASE IDENTICAL TO 1-AMINOCYCLOPROPANE-1- CARBOXYLATE OXIDASE (ACC OXIDASE) GB X66719 (EAT1). ESTS GB T43073, GB T5714, GB R90435, GB R44023, GB AA597926, GB AI099676, GB AA650810 AND GB 29725 COME FROM THIS GENE | Oxidase |
| 403 | 62 | O-GLCNAC TRANSFERASE SIMILAR TO RATTUS O- GLCNAC TRANSFERASE (GB U76557)[PUTATIVE] | Transferases |
| 412 | 63 | PEROXIDASE ATP12A STRONG SIMILARITY TO ARABIDOPSIS PEROXIDASE ATP11A (GB X98802)[PUTATIVE] | Oxidase |
| 413 | 64 | PEROXIDASE ATP12A STRONG SIMILARITY TO ARABIDOPSIS PEROXIDASE ATP11A (GB X98802)[PUTATIVE] | Oxidase |
| 414 | 65 | PEROXIDASE STRONG SIMILARITY TO ARABIDOPSIS PEROXIDASE ATPEROX7A (GB X98321)[PUTATIVE] | Oxidase |
| 418 | 66 | ZINC TRANSPORTER SIMILAR TO ARABIDOPSIS FE(II) TRANSPORT PROTEIN (GB U27590)[PUTATIVE] | Transporter |
| 419 | 67 | PECTIN METHYLESTERASE SIMILAR TO PRUNUS PECTINESTERASE (GB X95991)[PUTATIVE] | Esterase |
| 440 | 68 | UDP-GLUCOSE:INDOLE-3-ACETATE BETA-D- GLUCOSYLTRANSFERASE, PUTATIVE SIMILAR TO UDP-GLUCOSE:INDOLE-3-ACETATE BETA-D- GLUCOSYLTRANSFERASE GI:2149127 FROM [ARABIDOPSIS THALIANA] | Transferases |
| 443 | 69 | UDP-GLUCOSE:INDOLE-3-ACETATE BETA-D- GLUCOSYLTRANSFERASE, PUTATIVE SIMILAR TO UDP-GLUCOSE:INDOLE-3-ACETATE BETA-D- GLUCOSYLTRANSFERASE GI:2149127 FROM [ARABIDOPSIS THALIANA] | Transferases |

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| 444 | 70 | GLUCAN SYNTHASE HIGHLY SIMILAR TO PUTATIVE GLUCAN SYNTHASE GB:AAD15408[PUTATIVE] | Synthase |
| 445 | 71 | NA/H ANTIporter PROTEINS; N-TERMINAL HALF OF PROTEIN IS SIMILAR TO NA/H ANTIporter PROTEINS[HYPOTHETICAL PROTEIN SIMILAR TO] | Transporter |
| 452 | 72 | POLYGALACTURONASE SIMILAR TO GB:AAC23398[PUTATIVE] | Glycosylase |
| 453 | 73 | POLYGALACTURONASE SIMILAR TO GB:AAC23398[PUTATIVE] | Glycosylase |
| 454 | 74 | INDOLE-3-ACETATE BETA-GLUCOSYLTRANSFERASE SIMILAR TO INDOLE-3-ACETATE BETA- GLUCOSYLTRANSFERASE GB:AAD32293[PUTATIVE] | Transferases |
| 455 | 75 | INDOLE-3-ACETATE BETA-GLUCOSYLTRANSFERASE SIMILAR TO INDOLE-3-ACETATE BETA- GLUCOSYLTRANSFERASE GB:AAD32293[PUTATIVE] | Transferases |
| 466 | 76 | NPK1-RELATED PROTEIN KINASE 2 PREDICTED BY GENEMARK.HMM[PUTATIVE] | Kinase, Protein |
| 472 | 77 | CHITINASE, CLASS I, PUTATIVE SIMILAR TO GB:AAF69774 FROM [ARABIDOPSIS BLEPHAROPHYLLA] (PROC. NATL. ACAD. SCI. U.S.A. 97 (10), 5322-5327 (2000)) | Chitinase |
| 486 | 78 | UDPG GLUCOSYLTRANSFERASE GB:AAB62270 GI:2232354 FROM [SOLANUM BERTHAULTII], UNKNOWN PROTEIN CONTAINS SIMILARITY TO | Transferases |
| 488 | 79 | FRUCTOKINASE, PUTATIVE SIMILAR TO FRUCTOKINASE GB:U62329 GI:1915973 FROM [LYCOPERSICON ESCULENTUM] | Kinase |
| 489 | 80 | FRUCTOKINASE, PUTATIVE SIMILAR TO FRUCTOKINASE GB:U37838 GI:1052972 FROM [BETA VULGARIS] | Kinase |
| 494 | 81 | DELTA 9 DESATURASE IDENTICAL TO DELTA 9 DESATURASE GB:BAA25180 GI:2970034 FROM [ARABIDOPSIS THALIANA] | Desaturases |
| 495 | 82 | DELTA 9 DESATURASE, PUTATIVE SIMILAR TO DELTA 9 DESATURASE GB:BAA25180 GI:2970034 FROM [ARABIDOPSIS THALIANA] | Desaturases |

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| 496 | 83 | DELTA 9 DESATURASE, PUTATIVE SIMILAR TO DELTA 9 DESATURASE GB:BAA25180 GI:2970034 FROM [ARABIDOPSIS THALIANA] | Desaturases |
| 498 | 84 | DELTA 9 DESATURASE, PUTATIVE SIMILAR TO DELTA 9 DESATURASE GB:BAA25180 GI:2970034 FROM [ARABIDOPSIS THALIANA] | Desaturases |
| 511 | 85 | LIPASE-LIKE PROTEIN SIMILAR TO LIPASE GB:AAD01804 GI:4103627 FROM [DIANTHUS CARYOPHYLLUS] | Lipase |
| 520 | 86 | DELTA 9 DESATURASE, PUTATIVE SIMILAR TO DELTA 9 DESATURASE GI:2970034 FROM [ARABIDOPSIS THALIANA] | Desaturases |
| 521 | 87 | DELTA 9 DESATURASE, PUTATIVE SIMILAR TO DELTA 9 DESATURASE GI:2970034 FROM [ARABIDOPSIS THALIANA] | Desaturases |
| 532 | 88 | GLUCAN SYNTHASE, PUTATIVE SIMILAR TO GLUCAN SYNTHASE GB:AAD11794 [FILOBASIDIELLA NEOFORMANS VAR. NEOFORMANS] | Synthase |
| 544 | 89 | IRON/ASCORBATE OXIDOREDUCTASE FAMILY | Reductase |
| 546 | 90 | IRON/ASCORBATE OXIDOREDUCTASE FAMILY | Reductase |
| 547 | 91 | IRON/ASCORBATE OXIDOREDUCTASE FAMILY | Reductase |
| 552 | 92 | PROTEIN KINASE, 5' PARTIAL CONTAINS PFAM PROFILE: PF00069 EUKARYOTIC PROTEIN KINASE DOMAIN | Kinase, Protein |
| 555 | 93 | RIBOKINASE, SUGAR KINASE, PUTATIVE SIMILAR TO RIBOKINASE GB:AAD00536 GI:4099074 FROM [PYROBACULUM AEROPHILUM] | Kinase |
| 562 | 94 | LIPASE, PUTATIVE SIMILAR TO LIPASE GB:AAD01804 GI:4103627 FROM [DIANTHUS CARYOPHYLLUS] | Lipase |
| 564 | 95 | PHYTOENE DEHYDROGENASE RELATED ENZYME UNKNOWN PROTEIN CONTAINS PFAM PROFILE:PF02032 | Dehydrogenase |
| 566 | 96 | RECEPTOR PROTEIN KINASE, PUTATIVE SIMILAR TO RECEPTOR PROTEIN KINASE GB:BAA11869 GI:1389566 FROM [ARABIDOPSIS THALIANA] | Kinase, Protein |

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| 568 | 97 | PROCESSING PEPTIDASE, CHLOROPLAST THYLAKOIDAL PROCESSING PEPTIDASE, PUTATIVE SIMILAR TO CHLOROPLAST THYLAKOIDAL PROCESSING PEPTIDASE GB:CAA71502 GI:2769566 FROM [ARABIDOPSIS THALIANA] | Protease |
| 576 | 98 | NA ⁺ /H ⁺ ANTIporter GI:2347190 FROM [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN SIMILAR TO][PUTATIVE] | Transporter |
| 581 | 99 | MITOCHONDRIAL CARRIER PROTEINS[HYPOTHETICAL PROTEIN CONTAINS SIMILARITY TO] | Transporter |
| 596 | 100 | ALTERNATIVE NADH-DEHYDROGENASE GI:3718005 FROM [YARROWIA LIPOLYTICA] UNKNOWN PROTEIN CONTAINS SIMILARITY TO | Dehydrogenases |
| 597 | 101 | PROTEASE ATP-DEPENDENT [HYPOTHETICAL PROTEIN CONTAINS SIMILARITY TO] | Protease |
| 602 | 102 | UDP-GLUCOSE GLUCOSYLTRANSFERASE, PUTATIVE SIMILAR TO UDP-GLUCOSE GLUCOSYLTRANSFERASE GI:453245 FROM [MANIHOT ESCULENTA] | Transferases |
| 603 | 103 | UDP-GLUCOSE GLUCOSYLTRANSFERASE, PUTATIVE SIMILAR TO UDP-GLUCOSE GLUCOSYLTRANSFERASE GI:453245 FROM [MANIHOT ESCULENTA] | Transferases |
| 604 | 104 | UDP-GLUCOSE GLUCOSYLTRANSFERASE, PUTATIVE SIMILAR TO UDP-GLUCOSE GLUCOSYLTRANSFERASE GI:453245 FROM [MANIHOT ESCULENTA] | Transferases |
| 621 | 105 | PROTEIN PHOSPHATASE 2C, PUTATIVE SIMILAR TO GB:CAB90633 FROM [FAGUS SYLVATICA] | Phosphatase |
| 622 | 106 | TROPINONE REDUCTASE-I, PUTATIVE SIMILAR TO GB:L20473 FROM [DATURA STRAMONIUM] (PROC. NATL. ACAD. SCI. U.S.A. 90, 9591-9595 (1993)) | Reductase |
| 623 | 107 | TROPINONE REDUCTASE-I, PUTATIVE SIMILAR TO GB:L20473 FROM [DATURA STRAMONIUM] (PROC. NATL. ACAD. SCI. U.S.A. 90, 9591-9595 (1993)) | Reductase |
| 633 | 108 | PROTEIN KINASE, PUTATIVE CONTAINS PFAM PROFILE: PF00069, EUKARYOTIC PROTEIN KINASE DOMAIN (1 COPY) | Kinase, Protein |

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| 634 | 109 | PROTEIN KINASE, PUTATIVE CONTAINS PFAM PROFILE: PF00069 EUKARYOTIC PROTEIN KINASE DOMAIN (1 COPY) | Kinase, Protein |
| 642 | 110 | RECEPTOR-LIKE SERINE/THREONINE KINASE, PUTATIVE SIMILAR TO GB:AAC50043 FROM [ARABIDOPSIS THALIANA] (PLANT MOL. BIOL. 37 (4), 587-596 (1998)) | Kinase, Protein |
| 649 | 111 | FATTY ACID ELONGASE 3-KETOACYL-COA SYNTHASE, PUTATIVE SIMILAR TO GB:AAC99312 FROM [ARABIDOPSIS THALIANA] (PLANT J. (1999) IN PRESS) | Synthase |
| 653 | 112 | PHOSPHORIBOSYLANTHRANILATE ISOMERASE IDENTICAL TO GB:AAB03498 FROM [ARABIDOPSIS THALIANA] (CELL 83 (5), 725-734 (1995)) | Isomerase |
| 661 | 113 | PROTEIN KINASE, PUTATIVE (FRAGMENT) SIMILAR TO GB:BAA94509 FROM [POPULUS NIGRA] | Kinase, Protein |
| 663 | 114 | L-ASCORBATE PEROXIDASE IDENTICAL TO GB:CAA42168 FROM [ARABIDOPSIS THALIANA] (PLANT MOL. BIOL. 18 (4), 691-701 (1992)) | Oxidase |
| 683 | 115 | HIGH-AFFINITY NITRATE TRANSPORTER NRT2 IDENTICAL TO GB:CAB09794 FROM [ARABIDOPSIS THALIANA] | Transporter |
| 684 | 116 | HIGH-AFFINITY NITRATE TRANSPORTER ACH2 IDENTICAL TO GB:AAC35884 FROM [ARABIDOPSIS THALIANA] (PLANT J. 17 (5), 563-568 (1999)) | Transporter |
| 695 | 117 | DTDP-GLUCOSE 4-6-DEHYDRATASE GI:9759250 FROM [ARABIDOPSIS THALIANA] [UNKNOWN PROTEIN CONTAINS SIMILARITY TO] | Dehydratase |
| 696 | 118 | PROTEASE GI:4415912 FROM [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN SIMILAR TO][PUTATIVE] | Protease |
| 698 | 119 | AMINO ACID PERMEASE GI:7415521 FROM [ORYZA SATIVA][HYPOTHETICAL PROTEIN CONTAINS SIMILARITY TO] | Transporter |
| 699 | 120 | PREPHENATE DEHYDRATASE GI:1008717 FROM [AMYCOLATOPSIS METHANOLICA][HYPOTHETICAL PROTEIN CONTAINS SIMILARITY TO] | Dehydratase |

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| 702 | 121 | ALPHA2,8-SIALYLTRANSFERASE GI:929684 FROM [MUS MUSCULUS][HYPOTHETICAL PROTEIN CONTAINS SIMILARITY TO] | Transferases |
| 724 | 122 | ACYL-(ACYL CARRIER PROTEIN) THIOESTERASE, PUTATIVE ALMOST IDENTICAL TO ACYL-(ACYL CARRIER PROTEIN) THIOESTERASE GB:CAA85387 GI:634003 FROM [ARABIDOPSIS THALIANA] | Esterase |
| 725 | 123 | MG-CHELATASE, PUTATIVE SIMILAR TO MG-CHELATASE GB:AF014399 GI:2318116 FROM [PISUM SATIVUM] | Chelataze |
| 728 | 124 | VIOLAXANTHIN DE-EPOXIDASE PRECURSOR (U44133) SIMILAR TO EST GB N37612[PUTATIVE] | Oxidase |
| 732 | 125 | RECEPTOR KINASE, CLV1 SIMILAR TO RECEPTOR-LIKE PROTEIN KINASE (IPOMOEIA NIL) (U77888)[PUTATIVE] | Kinase, Protein |
| 739 | 126 | BETA-GALACTOSIDE ALPHA-2,3-SIALYLTRANSFERASE (PIR JC5251), UNKNOWN PROTEIN SIMILAR TO | Transferases |
| 761 | 127 | SUGAR TRANSPORT PROTEIN, ERD6 SIMILAR TO GB:BAA25989[PUTATIVE] | Transporter |
| 769 | 128 | AMIDASE (GB D16207). ESTS GB T20504,GB H36650,GB N97423,GB H36595 COME FROM THIS GENE; SIMILARITY TO | AMIDASE |
| 772 | 129 | BETA-MANNOSIDASE (GB U46067), UNKNOWN PROTEIN CONTAINS SIMILARITY TO BOS | Glycosylase |
| 773 | 130 | AMP-ACTIVATED PROTEIN KINASE (GB X95577)[HYPOTHETICAL PROTEIN CONTAINS SIMILARITY TO] RATTUS | Kinase, Protein |
| 785 | 131 | PROTEIN PHOSPHATASE 2C SIMILAR TO GB:AAC16260[PUTATIVE] | Phosphatase |
| 792 | 132 | NICOTIANAMINE SYNTHASE SIMILAR TO GB:BAA74589[PUTATIVE] | Synthase |
| 803 | 133 | GALACTINOL SYNTHASE SIMILAR TO GB:AAD26116 FROM [BRASSICA NAPUS][PUTATIVE] | Synthase |
| 807 | 134 | LIPASE SIMILAR TO NODULINS AND LIPASE; LOCATION OF EST E6C2T7 , GB AA042309. SIMILAR TO NODULINS GI 3328240, GI 2129854 AND OTHERS AND LIPASE, GI 2129636[PUTATIVE] | Lipase |

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| 808 | 135 | 12-OXOPHYTODIENOATE REDUCTASE OPRI SIMILAR TO 12-OXOPHYTODIENOATE REDUCTASE, GI 2765083 AND OLD-YELLOW-ENZYME HOMOLOG, GI 2232254[PUTATIVE] | Reductase |
| 812 | 136 | SER/THR PROTEIN KINASE SIMILAR TO GB:AAD21713[PUTATIVE] | Kinase, Protein |
| 814 | 137 | BETA-1,3-GLUCANASE GB:AAD22663, LOCATION OF EST 192N12T7, GB R90355, UNKNOWN PROTEIN SIMILAR TO | Glycosylase |
| 823 | 138 | PECTINACETYLESTERASE PRECURSOR SIMILAR TO VIGNA RADIATA PECTINACETYLESTERASE PRECURSOR, GI 1431629[PUTATIVE] | Esterase |
| 847 | 139 | PHYTOCHELATIN SYNTHETASE SIMILAR TO GB:CAA07251[PUTATIVE] | Synthase |
| 862 | 140 | GLUTAMYL-TRNA REDUCTASE 2 PRECURSOR SIMILAR TO GB:P49294 AND TO A. THALIANA HEMA2 (GB U27118)[PUTATIVE] | Reductase |
| 864 | 141 | SUCROSE/H+ SYMPORTER SIMILAR TO GB:CAA76367 AND VICIA SUCROSE TRANSPORT PROTEIN (GB Z93774)[PUTATIVE] | Transporter |
| 865 | 142 | RECEPTOR-LIKE PROTEIN KINASE | Kinase, Protein |
| 868 | 143 | REVERSE TRANSCRIPTASE SIMILAR TO GB:AAD29058[PUTATIVE] | Transcriptase |
| 869 | 144 | AMINO ACID PERMEASE GC SPLICE SITE AT POSITION 1256 IS PREDICTED FROM ALIGNMENT AND NOT CONFIRMED EXPERIMENTALLY. HIGHLY SIMILAR TO ARABIDOPSIS THALIANA AMINO ACID PERMEASE I GI 404019, AND OTHER AMINO ACID PERMEASES[PUTATIVE] | Transporter |
| 873 | 145 | XYLAN ENDOHYDROLASE SIMILAR TO GB:AAD27896 TO ENDOXYLANASES GI 1255238 (THERMOANAEROBACTERIUM THERMOSULFURIGENES), GI 1813595 (HORDEUM VULGARE) AND OTHERS[PUTATIVE] | Hydrolase |
| 894 | 146 | LECTIN RECEPTOR KINASE VERY SIMILAR TO GB:CAA69271[PUTATIVE] | Kinase, Protein |

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| 899 | 147 | OXIDOREDUCTASE IN MRPL44-MTF1 INTERGENIC PROTEIN (SP Q05016 YM71_YEAST [UNKNOWN PROTEIN SIMILAR TO DAUNORUBICIN C-13 (U77891); SIMILAR TO] | Reductase |
| 904 | 148 | GLUTATHIONE S-TRANSFERASE TSI-1 SIMILAR TO GLUTATHIONE S-TRANSFERASE (SP Q03666 GTX4_TOBAC); SIMILAR TO EST GB H36275[PUTATIVE] | Transferases |
| 905 | 149 | GLUTATHIONE S-TRANSFERASE TSI-1 SIMILAR TO GLUTATHIONE S-TRANSFERASE TSI-1 (GI 2190992); SIMILAR TO ESTS GB R29860, EMB Z29757, AND EMB Z29758[PUTATIVE] | Transferases |
| 907 | 150 | CELL RECEPTOR BETA CHAIN CDR3 (GI 3064031); SIMILAR TO NUCLEOPORIN NUP145 (SP P49687 N145_YEAST); SIMILAR TO ESTS GB N37877, EMB Z29159, AND EMB Z30865 | Receptor |
| 908 | 151 | GLUCOSYL TRANSFERASE SIMILAR TO IMMEDIATE-EARLY SALICYLATE-INDUCED GLUCOSYLTRANSFERASE (AC005167), PUTATIVE | Transferases |
| 913 | 152 | GERMIN-LIKE OXALATE OXIDASE SIMILAR TO ESTS GB T88481 AND GB AI099566 | Oxidase |
| 922 | 153 | ENDOXYLOGLUKAN TRANSFERASE SIMILAR TO XYLOGLUKAN ENDOTRANSGLYCOSYLASE-RELATED PROTEIN XTR4 (PIR IS71223)[PUTATIVE] | Transferases |
| 924 | 154 | TYROSINE PHOSPHATASE 2 SIMILAR TO PROTEIN-TYROSINE PHOSPHATASE 2 (GI 3249071), SIMILAR TO EST GB N96456[PUTATIVE] | Phosphatase |
| 929 | 155 | PROTEIN KINASE, PUTATIVE SIMILAR TO PROTEIN KINASE 1 GI:7573596 FROM [POPULUS NIGRA] | Kinase, Protein |
| 931 | 156 | POLYGALACTURONASE PG1, PUTATIVE SIMILAR TO POLYGALACTURONASE PG1 GI:5669846 FROM [GLYCINE MAX] | Glycosylase |
| 937 | 157 | PHOSPHORIBOSYL DIPHOSPHATE SYNTHASE STRONG SIMILARITY TO GI 4544471 F23E6.11 FROM ARABIDOPSIS THALIANA BAC GB AC006580[PUTATIVE] | Synthase |

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| 941 | 158 | LIPASE SIMILAR TO GB X02844 LIPASE PRECURSOR FROM STAPHYLOCOCCUS HYICUS. ESTS GB AI239406 AND GB T76725 COME FROM THIS GENE[PUTATIVE] | Lipase |
| 943 | 159 | PYRUVATE PHOSPHATE DIKINASE, PEP/PYRUVATE BINDING DOMAIN | Kinase |
| 948 | 160 | ALDO/KETO REDUCTASE FAMILY - AUXIN-INDUCED PROTEIN STRONG SIMILARITY TO GB X56267 AUXIN-INDUCED PROTEIN (PCNT115) FROM NICOTIANA TABACUM 00248[PUTATIVE] | Reductase |
| 952 | 161 | RECEPTOR KINASE, 3' PARTIAL IDENTICAL TO GB:AAB65490 | Kinase, Protein |
| 963 | 162 | ZIP4, A PUTATIVE ZINC TRANSPORTER PER SUGGESTION BY DR. NATASHA M. GROTZ (PNAS, VOL 95., 7220-7224) | Transporter |
| 969 | 163 | SER/THR PROTEIN KINASE ISOLOG | Kinase, Protein |
| 973 | 164 | LYSOPHOSPHOLIPASE ISOLOG | Lipase |
| 977 | 165 | LEUCINE-RICH REPEAT TRANSMEMBRANE PROTEIN KINASE, PUTATIVE SIMILAR TO LEUCINE-RICH REPEAT TRANSMEMBRANE PROTEIN KINASE GB:AAC27895 GI:3360291 FROM [ZEA MAYS] | Kinase, Protein |
| 981 | 166 | SECRETORY CARRIER MEMBRANE PROTEIN, PUTATIVE SIMILAR TO SECRETORY CARRIER MEMBRANE PROTEIN GB:AAF36686 GI:7109228 FROM [ARABIDOPSIS THALIANA] | Transporter |
| 982 | 167 | BIFUNCTIONAL NUCLEASE BFN1 ALMOST IDENTICAL TO BIFUNCTIONAL NUCLEASE BFN1 GB:AAD00693 GI:4099831 FROM [ARABIDOPSIS THALIANA] | Nuclease |
| 992 | 168 | SERINE/THREONINE KINASE, PUTATIVE SIMILAR TO SERINE/THREONINE KINASE GB:Y12530 GI:2181187 FROM [BRASSICA OLERACEA] | Kinase, Protein |
| 994 | 169 | SERINE/THREONINE KINASE, PUTATIVE SIMILAR TO SERINE/THREONINE KINASE GB:Y12531 GI:2181189 FROM [BRASSICA OLERACEA] | Kinase, Protein |
| 997 | 170 | RECEPTOR-LIKE PROTEIN KINASE, PUTATIVE SIMILAR TO RECEPTOR-LIKE PROTEIN KINASE GB:AAC95353 GI:4008010 FROM [ARABIDOPSIS THALIANA] | Kinase, Protein |

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| 998 | 171 | RECEPTOR KINASE, PUTATIVE SIMILAR TO RECEPTOR KINASE 1 GB:BAA23676 GI:2662048 FROM [BRASSICA RAPA] | Kinase, Protein |
| 1001 | 172 | PECTIN METHYLESTERASE, PUTATIVE SIMILAR TO PECTIN METHYLESTERASE GI:1279597 FROM [NICOTIANA PLUMBAGINIFOLIA] | Esterase |
| 1005 | 173 | RECEPTOR-LIKE KINASE, PUTATIVE SIMILAR TO RECEPTOR-LIKE KINASE GI:1783311 FROM [BRASSICA OLERACEA] | Kinase, Protein |
| 1008 | 174 | SERINE/THREONINE PROTEIN KINASE EMB CAA69216 CONTAINS SIMILARITY TO EXTENSIN PROTEIN GI:512380 FROM [BRASSICA NAPUS][SIMILAR TO] | Kinase, Protein |
| 1019 | 175 | ENDO-XYLOGLUCAN TRANSFERASE, PUTATIVE SIMILAR TO ENDO-XYLOGLUCAN TRANSFERASE GI:2244732 FROM [GOSSYPIMUM HIRSUTUM] | Transferases |
| 1022 | 176 | PECTIN METHYLESTERASE, PUTATIVE SIMILAR TO PECTIN METHYLESTERASE GI:1617583 FROM [LYCOPERSICON ESCULENTUM] | Esterase |
| 1023 | 177 | PECTIN METHYLESTERASE, PUTATIVE SIMILAR TO FRUIT-SPECIFIC PECTIN METHYLESTERASE GI:1617583 FROM [LYCOPERSICON ESCULENTUM] | Esterase |
| 1035 | 178 | GLYCOGEN SYNTHASE STRONG SIMILARITY TO GB X95759 SOLUBLE-STARCH-SYNTHASE PRECURSOR (SSIII) FROM SOLANUM TUBEROSUM[PUTATIVE] | Synthase |
| 1040 | 179 | RETICULINE OXIDASE STRONG SIMILARITY TO GB AF049347 BERBERINE BRIDGE ENZYME FROM BERBERIS STOLONIFERA[PUTATIVE] | Oxidase |
| 1042 | 180 | PREPHENATE DEHYDRATASE CHLOROPLAST SIMILAR TO GI 2392772 AND IS A MEMBER OF THE PF 00800 PREPHENATE DEHYDRATASE FAMILY. ESTS GB T21562 AND GB T21062 COME FROM THIS GENE[PUTATIVE] | Dehydratase |
| 1046 | 181 | BETA-1,3-GLUCANASE SIMILAR TO GLUCAN ENDO-1,3-BETA-D-GLUCOSIDASE PRECURSOR GB Z28697 FROM NICOTIANA TABACUM. ESTS GB Z18185 AND GB AA605362 COME FROM THIS GENE[PUTATIVE] | Glycosylase |

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| 1047 | 182 | LACTOYLGLUTATHIONE LYASE-LIKE PROTEIN SIMILAR TO PROTEIN GB Z74962 FROM BRASSICA OLERACEA WHICH IS SIMILAR TO BACTERIAL YRN1 AND HEAHIO PROTEINS. ESTS GB T21954, GB T04283, GB Z37609, GB N37366, GB R90704, GB F15500 AND GB F14353 COME FROM THIS GENE | Lyase |
| 1055 | 183 | PECTATE LYASE-LIKE PROTEIN SIMILAR TO STYLE DEVELOPMENT-SPECIFIC PROTEIN 9612 PRECURSOR GB X55193 AND PECTATE LYASE P59 PRECURSOR GB X15499 FROM LYCOPERSICON ESCULENTUM | Lyase |
| 1063 | 184 | PYROPHOSPHATE-FRUCTOSE-6-PHOSPHATE PHOSPHOTRANSFERASE SIMILAR TO PYROPHOSPHATE-DEPENDENT PHOSPHOFUCTOKINASE BETA SUBUNIT GB Z32850 FROM RICINUS COMMUNIS. ESTS GB N65773, GB N64925 AND GB F15232 COME FROM THIS GENE[PUTATIVE] | 1-Transferases |
| 1064 | 185 | 1-AMINO-CYCLOPROPANE-CARBOXYLIC ACID OXIDASE (ACC OXIDASE) STRONG SIMILARITY TO AMINO-CYCLOPROPANE-CARBOXYLIC ACID OXIDASE GB L27664 FROM BRASSICA NAPUS. ESTS GB Z48548 AND GB Z48549 COME FROM THIS GENE[PUTATIVE] | Oxidase |
| 1158 | 186 | NITRATE TRANSPORTER, PUTATIVE SIMILAR TO GB:CAB09794 FROM [ARABIDOPSIS THALIANA] | Transporter |
| 1163 | 187 | BETA-1,4-N-ACETYLGLUCOSAMINYLTRANSFERASE CONTAINS SIMILARITY TO GI 4417304 F15011.7 PUTATIVE BETA-1,4-MANNOSYL-GLYCOPROTEIN BETA-1,4-N-ACETYLGLUCOSAMINYLTRANSFERASE FROM ARABIDOPSIS THALIANA BAC GB AC006446[PUTATIVE] | Transferases |
| 1170 | 188 | CYTOCHROME P450 MONOOXYGENASE STRONG SIMILARITY TO GB D78605 CYTOCHROME P450 MONOOXYGENASE FROM ARABIDOPSIS THALIANA AND IS A MEMBER OF THE PF 00067 CYTOCHROME P450 FAMILY[PUTATIVE] | Oxygenases |

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| 1177 | 189 | CYTOCHROME P450 MONOOXYGENASE STRONG SIMILARITY TO GI 3313615 F2IJ9.9 FROM ARABIDOPSIS THALIANA AND IS A MEMBER OF THE PF 00067 CYTOCHROME P450 FAMILY[PUTATIVE] | Oxygenases |
| 1187 | 190 | GLYCOSYL TRANSFERASE GI:6862930 FROM [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN SIMILAR TO][PUTATIVE] | Transferases |
| 1190 | 191 | ALLENE OXIDE CYCLASE, PUTATIVE SIMILAR TO ALLENE OXIDE CYCLASE GI:8977961 FROM [LYCOPERSICON ESCULENTUM] | Cyclase |
| 1204 | 192 | STEROID SULFOTRANSFERASE, PUTATIVE SIMILAR TO STEROID SULFOTRANSFERASE 1 GI:3420004 FROM [BRASSICA NAPUS] | Transferases |
| 1220 | 193 | NADPH-CYTOCHROME P450 REDUCTASE GI:10442765 FROM [TRITICUM AESTIVUM][HYPOTHETICAL PROTEIN CONTAINS SIMILARITY TO] | Reductase |
| 1241 | 194 | 2-HYDROXY-6-OXO-7-METHYLOCTA-2,4-DIENOATE HYDROLASE GI:2822275 FROM [PSEUDOMONAS PUTIDA], UNKNOWN PROTEIN CONTAINS SIMILARITY TO | Hydrolase |
| 1242 | 195 | BETA 1,3-GLUCANASE (GLC1) GI:924952 FROM [TRITICUM AESTIVUM][HYPOTHETICAL PROTEIN CONTAINS SIMILARITY TO] | Glycosylase |
| 1260 | 196 | RIBULOSE-1,5 BISPHOSPHATE CARBOXYLASE/OXYGENASE LARGE SUBUNIT N-METHYLTRANSFERASE HIGHLY SIMILAR TO RIBULOSE-1,5 BISPHOSPHATE CARBOXYLASE/OXYGENASE LARGE SUBUNIT N-METHYLTRANSFERASE, GI 1731475. RARE GC INTRON SPLICE SITE AT 49572 IS INFERRED FROM PROTEIN ALIGNMENT AND IS NOT CONFIRMED EXPERIMENTALLY[PUTATIVE] | Transferases |
| 1263 | 197 | XYLOGLUCAN FUCOSYLTRANSFERASE, PUTATIVE SIMILAR TO XYLOGLUCAN FUCOSYLTRANSFERASE GI:5231145 FROM [ARABIDOPSIS THALIANA] | Transferases |
| 1265 | 198 | LIPOAMIDE DEHYDROGENASE, PUTATIVE | Dehydrogenases |

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| 1268 | 199 | 2-OXOACID DEPENDENT DIOXYGENASE, DIOXYGENASE-LIKE PROTEIN VERY SIMILAR TO ADVENTITIOUS ROOTING RELATED OXYGENASE; VERY SIMILAR TO 2-OXOACID DEPENDENT DIOXYGENASE FROM MALUS DOMESTICA, GI3492806 | Oxygenases |
| 1269 | 200 | 2-OXOACID DEPENDENT DIOXYGENASE, DIOXYGENASE-LIKE PROTEIN VERY SIMILAR TO ADVENTITIOUS ROOTING RELATED OXYGENASE; VERY SIMILAR TO 2-OXOACID DEPENDENT DIOXYGENASE FROM MALUS DOMESTICA, GI3492806 | Oxygenases |
| 1274 | 201 | MANDELONITRILE LYASE SIMILAR TO MANDELONITRILE LYASES GB:P52707, P52706, AND O50048; CONTAINS MC OXIDOREDUCTASES PROTEIN MOTIF[PUTATIVE] | Reductase |
| 1275 | 202 | MANDELONITRILE LYASE SIMILAR TO MANDELONITRILE LYASES GB:P52707, P52706, AND O50048; CONTAINS MC OXIDOREDUCTASES PROTEIN MOTIF[PUTATIVE] | Reductase |
| 1277 | 203 | RIBONUCLEASE CONTAINS RIBONUCLEASE T2 FAMILY HISTIDINE PROTEIN MOTIF[PUTATIVE] | Nuclease |
| 1278 | 204 | RIBONUCLEASE CONTAINS RIBONUCLEASE T2 FAMILY HISTIDINE PROTEIN MOTIF[PUTATIVE] | Nuclease |
| 1281 | 205 | NUCLEOSIDE TRIPHOSPHATASE, 3' PARTIAL SIMILAR TO GB:AAC32915[PUTATIVE] | Phosphatase |
| 1284 | 206 | ACID PHOSPHATASE, PUTATIVE SIMILAR TO ACID PHOSPHATASE GI:5360721 FROM [LUPINUS ALBUS] | Phosphatase |
| 1294 | 207 | RECEPTOR-LIKE PROTEIN KINASE GI:2947063 FROM [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN SIMILAR TO][PUTATIVE] | Kinase, Protein |
| 1297 | 208 | PECTATE LYASE, PUTATIVE SIMILAR TO PECTATE LYASE GI:2463509 FROM [ZINNIA ELEGANS] | Lyase |
| 1298 | 209 | GLYOXAL OXIDASE GI:399594 FROM [PHANEROCHAETE CHRYSOSPORIUM][HYPOTHETICAL PROTEIN CONTAINS SIMILARITY TO] | Oxidase |

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| 1301 | 210 | DNA POLYMERASE III GAMMA AND TAU SUBUNITS[HYPOTHETICAL PROTEIN CONTAINS SIMILARITY TO] | Polymerase |
| 1309 | 211 | ANIONIC PEROXIDASE, PUTATIVE SIMILAR TO ANIONIC PEROXIDASE GI:170202 FROM [NICOTIANA SYLVESTRIS] | Oxidase |
| 1310 | 212 | ANIONIC PEROXIDASE, PUTATIVE SIMILAR TO ANIONIC PEROXIDASE GI:170202 FROM [NICOTIANA SYLVESTRIS] | Oxidase |
| 1321 | 213 | NA ⁺ /H ⁺ ANTIporter, PUTATIVE SIMILAR TO NA ⁺ /H ⁺ ANTIporter GB:CAA69925 GI:1655702 FROM [XENOPUS LAEVIS] | Transporter |
| 1326 | 214 | PURPLE ACID PHOSPHATASE, PUTATIVE CONTAINS PFAM PROFILE: PF02227 PURPLE ACID PHOSPHATASE | Phosphatase |
| 1328 | 215 | XYLOGLUCAN ENDO-TRANSGLYCOSYLASE, PUTATIVE SIMILAR TO XYLOGLUCAN ENDO-TRANSGLYCOSYLASE GB:CAA63553 GI:1769907 [ARABIDOPSIS THALIANA], IDENTICAL TO ENDOXYLOGLUCAN TRANSFERASE RELATED PROTEIN GB:BAA20290, GI:2154611 [ARABIDOPSIS THALIANA] | Transferases |
| 1337 | 216 | ASPARTATE-SEMIALDEHYDE DEHYDROGENASE, PUTATIVE SIMILAR TO ASPARTATE-SEMIALDEHYDE DEHYDROGENASE SP:Q31219 [LEGIONELLA PNEUMOPHILA] | Dehydrogenases |
| 1345 | 217 | PECTINESTERASE GB:X85216 GI:732912 [PHASEOLUS VULGARIS]; UNKNOWN PROTEIN SIMILAR TO | Esterase |
| 1361 | 218 | GLUTAMINE AMIDOTRANSFERASE CLASS-I HISTONE ACETYLTRANSFERASE HAT B HYPOTHETICAL PROTEIN CONTAINS PFAM PROFILE: PF00117 | Transferases |
| 1362 | 219 | GLYCEROL KINASE IDENTICAL TO SP:P34893 FROM [ARABIDOPSIS THALIANA] (J. MOL. BIOL. 251 (4), 533-549 (1995))[PUTATIVE] | Kinase |
| 1370 | 220 | FAD/NADH-BINDING DOMAIN. ESTS GB H76345 AND GB AA651465 COME FROM THIS GENE | Reductase |
| 1389 | 221 | CYSTATHIONINE BETA SYNTHASE DOMAIN [HYPOTHETICAL PROTEIN SIMILAR TO] | Synthase |

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| 1409 | 222 | RECEPTOR LECTIN KINASE, PUTATIVE SIMILAR TO RECEPTOR LECTIN KINASE 3 GI:4100060 FROM [ARABIDOPSIS THALIANA] | Kinase, Protein |
| 1410 | 223 | OXIDOREDUCTASE GI:6751707 FROM [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN SIMILAR TO][PUTATIVE] | Reductase |
| 1411 | 224 | GIBBERELLIN 3 BETA-HYDROXYLASE, PUTATIVE SIMILAR TO GIBBERELLIN 3 BETA-HYDROXYLASE GI:3982753 FROM [ARABIDOPSIS THALIANA] | Hydroxylase |
| 1424 | 225 | INORGANIC PYROPHOSPHATASE, PUTATIVE SIMILAR TO INORGANIC PYROPHOSPHATASE GI:790478 FROM [NICOTIANA TABACUM] | Phosphatase |
| 1450 | 226 | CINNAMOYL COA REDUCTASE, PUTATIVE SIMILAR TO CINNAMOYL COA REDUCTASE GI:2058310 FROM [EUCALYPTUS GUNNII] | Reductase |
| 1454 | 227 | CYCLIC NUCLEOTIDE AND CALMODULIN-REGULATED ION CHANNEL PROTEIN, PUTATIVE SIMILAR TO CYCLIC NUCLEOTIDE AND CALMODULIN-REGULATED ION CHANNEL PROTEIN GI:4581207 FROM [ARABIDOPSIS THALIANA] | Channel |
| 1464 | 228 | WALL-ASSOCIATED KINASE 2 GI:4826399 FROM [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN CONTAINS SIMILARITY TO] | Kinase, Protein |
| 1465 | 229 | WALL-ASSOCIATED KINASE 2 GI:4826399 FROM [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN CONTAINS SIMILARITY TO] | Kinase, Protein |
| 1466 | 230 | WALL-ASSOCIATED KINASE 4 GI:3355308 FROM [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN CONTAINS SIMILARITY TO] | Kinase, Protein |
| 1467 | 231 | SERINE/THREONINE-SPECIFIC PROTEIN KINASE GI:7270012 FROM [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN SIMILAR TO][PUTATIVE] | Kinase, Protein |
| 1468 | 232 | WALL-ASSOCIATED KINASE 4 GI:3355308 FROM [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN CONTAINS SIMILARITY TO] | Kinase, Protein |

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| 1469 | 233 | WALL-ASSOCIATED KINASE 4 GI:3355308 FROM [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN CONTAINS SIMILARITY TO] | Kinase, Protein |
| 1470 | 234 | WALL-ASSOCIATED KINASE 4 GI:3355308 FROM [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN CONTAINS SIMILARITY TO] | Kinase, Protein |
| 1475 | 235 | PROTEIN PHOSPHATASE 2C SIMILAR TO GB:AAC36699[PUTATIVE] | Phosphatase |
| 1479 | 236 | WALL-ASSOCIATED KINASE SIMILAR TO GB AJ012423 WALL-ASSOCIATED KINASE 2 FROM ARABIDOPSIS THALIANA[PUTATIVE] | Kinase, Protein |
| 1487 | 237 | 3-DEOXY-D-MANNO-2-OCTULOSONATE-8-PHOSPHATE SYNTHASE SIMILAR TO GB Y14272 3-DEOXY-D-MANNO-2-OCTULOSONATE-8-PHOSPHATE SYNTHASE FROM PISUM SATIVUM[PUTATIVE] | Synthase |
| 1491 | 238 | NA/H ANTIporter SIMILAR TO GI 4835769 T8K14.18 PUTATIVE NA/H ANTIporter ISOLOG FROM ARABIDOPSIS THALIANA BAC GB AC007202[PUTATIVE] | Transporter |
| 1514 | 239 | RECEPTOR-LIKE SERINE/THREONINE KINASE, PUTATIVE SIMILAR TO RECEPTOR-LIKE SERINE/THREONINE KINASE GI:2465923 FROM [ARABIDOPSIS THALIANA] | Kinase, Protein |
| 1525 | 240 | INORGANIC PYROPHOSPHATASE, PUTATIVE SIMILAR TO VACUOLAR-TYPE H ⁺ -TRANSLOCATING INORGANIC PYROPHOSPHATASE GI:6901678 FROM [ARABIDOPSIS THALIANA] | Phosphatase |
| 1529 | 241 | H ⁺ -ATPASE CATALYTIC SUBUNIT, PUTATIVE SIMILAR TO H ⁺ -ATPASE CATALYTIC SUBUNIT GI:6518112 FROM [CITRUS UNSHIU] | ATPase |
| 1546 | 242 | SRG1-LIKE PROTEIN STRONG HOMOLOGY TO SRG1 PROTEIN, A NEW MEMBER OF THE FE(II)/ASCORBATE OXIDASE SUPERFAMILY, 73% IDENTICAL TO SRG1 [ARABIDOPSIS THALIANA] (GI 479047). LOCATION OF ESTS 147E17T7 (GB T76176) AND 136D2T7 (GB T45959) | Oxidase |

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| 1547 | 243 | SRG1-LIKE PROTEIN STRONG HOMOLOGY TO SRG1 PROTEIN, A NEW MEMBER OF THE FE(II)/ASCORBATE OXIDASE SUPERFAMILY, SIMILAR TO SRG1 PROTEIN [ARABIDOPSIS THALIANA] (GI 629561). LOCATION OF EST F1A5T7 (GB N96370) | Oxidase |
| 1560 | 244 | POLYGALACTURONASE AFTER FIRST 29 AMINO ACIDS, 43% IDENTICAL TO POLYGALACTURONASE [MEDICAGO SATIVA] (GI 3413322)[PUTATIVE] | Glycosylase |
| 1561 | 245 | RIBOKINASE [PUTATIVE] | Kinase |
| 1562 | 246 | GLUTATHIONE TRANSFERASE ONE OF THREE REPEATED PUTATIVE GLUTATHIONE TRANSFERASES. 72% IDENTICAL TO GLUTATHIONE TRANSFERASE [ARABIDOPSIS THALIANA] (GI 4006934)[PUTATIVE] | Transferases |
| 1563 | 247 | GLUTATHIONE TRANSFERASE SECOND OF THREE REPEATED PUTATIVE GLUTATHIONE TRANSFERASES. 72% IDENTICAL TO GLUTATHIONE TRANSFERASE [ARABIDOPSIS THALIANA] (GI 4006934). LOCATION OF ESTS 191A10T7 (GB R90188) AND 171N13T7 (GB R65532)[PUTATIVE] | Transferases |
| 1564 | 248 | GLUTATHIONE TRANSFERASE ONE OF THREE REPEATED GLUTATHIONE TRANSFERASES. 65% IDENTICAL TO GLUTATHIONE TRANSFERASE [ARABIDOPSIS THALIANA] (GI 4006934). LOCATION OF EST 141C5T7 (GB T46669)[PUTATIVE] | Transferases |
| 1568 | 249 | LEUCINE-RICH RECEPTOR PROTEIN KINASE 34% IDENTICAL TO LEUCINE-RICH RECEPTOR-LIKE PROTEIN KINASE [IPOMOEA NIL] (GI 1684913) AND 35% IDENTICAL TO LEUCINE-RICH RECEPTOR-LIKE PROTEIN KINASE [MALUS DOMESTICA] (GI 3641252)[PUTATIVE] | Kinase, Protein |
| 1569 | 250 | RECEPTOR PROTEIN KINASE APPROXIMATELY 30% IDENTICAL TO DISEASE RESISTANCE GENES [LYCOPERSICON PIMPINELLIFOLIUM] (GI 1184077 AND GI 1184075) AND [LYCOPERSICON ESCULENTUM] (GI 3894387 AND GI 3894393)[PUTATIVE] | Kinase, Protein |

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| 1570 | 251 | RECEPTOR PROTEIN KINASE APPROXIMATELY 30% IDENTICAL TO DISEASE RESISTANCE PROTEINS [LYCOPERSICON ESCULENTUM] (GI 3894387 AND GI 3894393) AND [LYCOPERSICON PIMPINELLIFOLIUM] (GI 1184075 AND GI 1184077)[PUTATIVE] | Kinase, Protein |
| 1584 | 252 | NON-LTR RETROELEMENT REVERSE TRANSCRIPTASE GB:AAD22368 GI:4544460 FROM [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN SIMILAR TO][PUTATIVE] | Transcriptase |
| 1600 | 253 | PROTEIN PHOSPHATASE 2C, PUTATIVE SIMILAR TO PROTEIN PHOSPHATASE 2C GI:3242077 FROM [ARABIDOPSIS THALIANA] | Phosphatase |
| 1601 | 254 | PROTEIN PHOSPHATASE 2C, PUTATIVE SIMILAR TO PROTEIN PHOSPHATASE 2C GI:3242077 FROM [ARABIDOPSIS THALIANA] | Phosphatase |
| 1618 | 255 | RECEPTOR-LIKE PROTEIN KINASE, PUTATIVE SIMILAR TO RECEPTOR-LIKE PROTEIN KINASE INRPK1 GI:1684913 FROM [IPOMOEA NIL] | Kinase, Protein |
| 1634 | 256 | WALL-ASSOCIATED KINASE 4 GI:3355308 FROM [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN CONTAINS SIMILARITY TO] | Kinase, Protein |
| 1642 | 257 | 12-OXOPHYTODIENOATE REDUCTASE, PUTATIVE SIMILAR TO 12-OXOPHYTODIENOATE REDUCTASE OPR1 GI:3882355 FROM [ARABIDOPSIS THALIANA] | Reductase |
| 1644 | 258 | 12-OXOPHYTODIENOATE REDUCTASE, PUTATIVE SIMILAR TO 12-OXOPHYTODIENOATE REDUCTASE GI:4894182 FROM [LYCOPERSICON ESCULENTUM] | Reductase |
| 1653 | 259 | THREONYL-TRNA SYNTHETASES [HYPOTHETICAL PROTEIN CONTAINS SIMILARITY TO] | |
| 1657 | 260 | PEPTIDYL-PROLYL CIS-TRANS ISOMERASE FKBP-TYPE, UNKNOWN PROTEIN CONTAINS PFAM PROFILE: PF00254 | Isomerase |
| 1669 | 261 | BETA-GLUCAN-ELICITOR RECEPTOR, PUTATIVE SIMILAR TO BETA-GLUCAN-ELICITOR RECEPTOR GB:D78510 GI:1752733 FROM [GLYCINE MAX] | Receptor |

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| 1674 | 262 | LYSOPHOSPHOLIPASE HOMOLOG, PUTATIVE SIMILAR TO LYSOPHOSPHOLIPASE HOMOLOG GB:AAB97366 GI:2801536 FROM [ORYZA SATIVA] | Lipase |
| 1681 | 263 | PEPTIDYL-TRNA HYDROLASE GB:D64003 GI:1001200 FROM [SYNECHOCYSTIS SP][HYPOTHETICAL PROTEIN CONTAINS SIMILARITY TO] | Hydrolase |
| 1683 | 264 | LIPASE GB:AAF36744 GI:7109480 FROM [ARABIDOPSIS THALIANA]; UNKNOWN PROTEIN SIMILAR TO PUTATIVE | Lipase |
| 1687 | 265 | 2-ISOPROPYLMALATE SYNTHASE, PUTATIVE SIMILAR TO 2-ISOPROPYLMALATE SYNTHASE GB:AF004165 GI:2213881 FROM [LYCOPERSICON PENNELLII] | Synthase |
| 1695 | 266 | GLYCOSYL TRANSFERASE FAMILY 8, HYPOTHETICAL PROTEIN CONTAINS PFAM PROFILE: PF01501 | Transferases |
| 1696 | 267 | FLAVONOL 4'-SULFOTRANSFERASE, PUTATIVE SIMILAR TO FLAVONOL 4'-SULFOTRANSFERASE GI:168168 FROM [FLAVERIA CHLORAEFOLIA] | Transferases |
| 1702 | 268 | BETA-1,3-GLUCANASE-LIKE PROTEIN GI:9758115 FROM [ARABIDOPSIS THALIANA], UNKNOWN PROTEIN SIMILAR TO | Glycosylase |
| 1705 | 269 | REVERSE TRANSCRIPTASE DNA DEPENDENT GI:2920563 FROM [SPRAGUEA LOPHII], UNKNOWN PROTEIN CONTAINS SIMILARITY TO | Transcriptase |
| 1706 | 270 | ALPHA GALACTOSYLTRANSFERASE, PUTATIVE SIMILAR TO ALPHA GALACTOSYLTRANSFERASE GI:5702018 FROM [TRIGONELLA FOENUM-GRACUM] | Transferases |
| 1723 | 271 | ISOCHORISMATE SYNTHASE, PUTATIVE SIMILAR TO ISOCHORISMATE SYNTHASE GI:3348077 FROM [ARABIDOPSIS THALIANA] | Synthase |
| 1739 | 272 | NON-LTR RETROELEMENT REVERSE TRANSCRIPTASE GI:4006833 FROM [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN SIMILAR TO][PUTATIVE] | Transcriptase |
| 1743 | 273 | NON-LTR RETROELEMENT REVERSE TRANSCRIPTASE GI:3738337 FROM [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN SIMILAR TO][PUTATIVE] | Transcriptase |

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| 1745 | 274 | RECEPTOR-LIKE SERINE/THREONINE KINASE, PUTATIVE SIMILAR TO RECEPTOR-LIKE SERINE/THREONINE . KINASE GI:2465925 FROM [ARABIDOPSIS THALIANA] | Kinase, Protein |
| 1753 | 275 | POLYGALACTURONASE-LIKE PROTEIN GI:10177371 FROM [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN SIMILAR TO] | Glycosylase |
| 1774 | 276 | WALL-ASSOCIATED KINASE 2, PUTATIVE SIMILAR TO GB:CAB42872 FROM [ARABIDOPSIS THALIANA] (PLANT MOL. BIOL. 39 (6), 1189-1196 (1999)) | Kinase, Protein |
| 1788 | 277 | 2-HYDROXYISOFLAVONE REDUCTASE, PUTATIVE SIMILAR TO PIR:T08106 FROM [BETULA PENDULA] | Reductase |
| 1789 | 278 | GSH-DEPENDENT DEHYDROASCORBATE REDUCTASE 1, PUTATIVE SIMILAR TO GB:BAA90672 FROM [ORYZA SATIVA] | Reductase |
| 1790 | 279 | GSH-DEPENDENT DEHYDROASCORBATE REDUCTASE 1, PUTATIVE SIMILAR TO GB:BAA90672 FROM [ORYZA SATIVA] | Reductase |
| 1793 | 280 | RIBOKINASE, PUTATIVE SIMILAR TO GB:AAD00536 FROM [PYROBACULUM AEROPHILUM] | Kinase |
| 1808 | 281 | PROTEASE LA (LON) ATP-DEPENDENT DOMAIN | Protease |
| 1812 | 282 | CYCLIC NUCLEOTIDE AND CALMODULIN-REGULATED ION CHANNEL PROTEIN, PUTATIVE SIMILAR TO CYCLIC NUCLEOTIDE AND CALMODULIN-REGULATED ION CHANNEL GI:4581207 FROM [ARABIDOPSIS THALIANA] | Channel |
| 1836 | 283 | FERREDOXIN-NADP REDUCTASE PRECURSOR, PUTATIVE SIMILAR TO GB:M25528 FROM [MESEMBRYANTHEMUM CRYSTALLINUM] | Reductase |
| 1838 | 284 | C-8,7 STEROL ISOMERASE IDENTICAL TO GB:AAD03489 FROM [ARABIDOPSIS THALIANA] (PLANT MOL. BIOL. 38 (5), 807-815 (1998)) | Isomerase |
| 1848 | 285 | SUBTILISIN PROTEASE | Protease |
| 1849 | 286 | SUBTILISIN PROTEASE | Protease |

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| 1863 | 287 | S-ADENOSYL-METHIONINE-STEROL-C-METHYLTRANSFERASE IDENTICAL TO STEROL-C-METHYLTRANSFERASE GI:1061040 FROM [ARABIDOPSIS THALIANA] | Transferases |
| 1894 | 288 | PROTEIN KINASE, PUTATIVE SIMILAR TO PROTEIN KINASE GI:2852447 FROM [ARABIDOPSIS THALIANA] | Kinase, Protein |
| 1911 | 289 | SUGAR TRANSPORTER PROTEIN NEARLY IDENTICAL TO ARABIDOPSIS SUGAR TRANSPORTER, GI:1495273[PUTATIVE] | Transporter |
| 1913 | 290 | INORGANIC PHOSPHATE TRANSPORTER PROTEIN SIMILAR TO GB:CAA67395[PUTATIVE] | Transporter |
| 1922 | 291 | PHOSPHOFRUCTO-1-KINASE, PYROPHOSPHATE-DEPENDENT PHOSPHOFRUCTOKINASE ALPHA SUBUNIT SIMILAR TO GB:AAC67587 FROM [CITRUS X PARADISI] AND GB:Q41140 FROM [RICINUS COMMUNIS][PUTATIVE] | Kinase |
| 1937 | 292 | O-METHYLTRANSFERASE, PUTATIVE SIMILAR TO GB:AAF28353 FROM [FRAGARIA X ANANASSA] | Transferases |
| 1938 | 293 | O-METHYLTRANSFERASE, PUTATIVE SIMILAR TO GB:AAF28353 FROM [FRAGARIA X ANANASSA] | Transferases |
| 1939 | 294 | ATPASE SIMILAR TO GB:AAF28353 FROM [FRAGARIA X ANANASSA][PUTATIVE] | ATPase |
| 1940 | 295 | O-METHYLTRANSFERASE, PUTATIVE SIMILAR TO GB:AAF28353 FROM [FRAGARIA X ANANASSA] | Transferases |
| 1959 | 296 | NON-LTR RETROELEMENT REVERSE TRANSCRIPTASE GB:AAC63678 GI:3738337 FROM [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN SIMILAR TO][PUTATIVE] | Transcriptase |
| 1968 | 297 | FLAVIN-CONTAINING MONOOXYGENASES, PUTATIVE IDENTICAL TO PUTATIVE FLAVIN-CONTAINING MONOOXYGENASES GB:AAF87896 GI:9454573 FROM [ARABIDOPSIS THALIANA] | Oxygenases |
| 1969 | 298 | CARBOXYVINYL-CARBOXYPHOSPHONATE PHOSPHORYLMUTASE GB:O49290 FROM [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN SIMILAR TO] | Mutase |

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| 1988 | 299 | SECA-TYPE CHLOROPLAST PROTEIN TRANSPORT FACTOR SIMILAR TO GB X82404 CHLOROPLAST SECA PROTEIN FROM PISUM.SATIVUM[PUTATIVE] | Transporter |
| 2007 | 300 | PECTINESTERASE, PUTATIVE SIMILAR TO PECTINESTERASE GB:CAB08077 GI:1944575 FROM [LYCOPERSICON ESCULENTUM] | Esterase |
| 2008 | 301 | PECTINESTERASE, PUTATIVE SIMILAR TO PECTINESTERASE GB:CAB08077 GI:1944575 FROM [LYCOPERSICON ESCULENTUM] | Esterase |
| 2014 | 302 | PHOSPHATIDYLINOSITOL-4-PHOSPHATE 5-KINASE, PUTATIVE SIMILAR TO PHOSPHATIDYLINOSITOL-4-PHOSPHATE 5-KINASE GB:CAB53377 GI:5777366 FROM [ARABIDOPSIS THALIANA] | Kinase |
| 2044 | 303 | TREHALOSE-6-PHOSPHATE PHOSPHATASE, PUTATIVE SIMILAR TO TREHALOSE-6-PHOSPHATE PHOSPHATASE GI:2944180 FROM [ARABIDOPSIS THALIANA] | Phosphatase |
| 2051 | 304 | PROTEIN PHOSPHATASE TYPE 2C, PUTATIVE SIMILAR TO PROTEIN PHOSPHATASE TYPE 2C GI:4336436 FROM [LOTUS JAPONICUS] | Phosphatase |
| 2056 | 305 | UDP-GLUCOSE GLUCOSYLTRANSFERASE, PUTATIVE SIMILAR TO UDP-GLUCOSE GLUCOSYLTRANSFERASE GI:3928543 FROM [ARABIDOPSIS THALIANA] | Transferases |
| 2057 | 306 | UDP-GLUCOSE GLUCOSYLTRANSFERASE IDENTICAL TO UDP-GLUCOSE GLUCOSYLTRANSFERASE GI:3928543 FROM [ARABIDOPSIS THALIANA] | Transferases |
| 2058 | 307 | UDP-GLUCOSE GLUCOSYLTRANSFERASE, PUTATIVE SIMILAR TO UDP-GLUCOSE GLUCOSYLTRANSFERASE GI:3928543 FROM [ARABIDOPSIS THALIANA] | Transferases |
| 2059 | 308 | UDP-GLUCOSE GLUCOSYLTRANSFERASE, PUTATIVE, 5' PARTIAL SIMILAR TO UDP-GLUCOSE GLUCOSYLTRANSFERASE GI:3928543 FROM [ARABIDOPSIS THALIANA] | Transferases |
| 2060 | 309 | UDP-GLUCOSE GLUCOSYLTRANSFERASE, PUTATIVE SIMILAR TO UDP-GLUCOSE GLUCOSYLTRANSFERASE GI:6561805 FROM [SORGHUM BICOLOR] | Transferases |

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| 2079 | 310 | PHOSPHORIBOSYLANTHRANILATE TRANSFERASE, PUTATIVE SIMILAR TO PHOSPHORIBOSYLANTHRANILATE TRANSFERASE GI:1396053 FROM [PISUM SATIVUM] | Transferases |
| 2084 | 311 | TRNA ADENYLYLTRANSFERASE SIMILAR TO TRNA ADENYLYLTRANSFERASE GB U15930 FROM LUPINUS ALBUS. EST GB AA721797 COMES FROM THIS GENE[PUTATIVE] | Transferases |
| 2089 | 312 | SUCROSE TRANSPORT PROTEIN, SUC2 STRONG SIMILARITY TO GB:S38196 SUCROSE TRANSPORT PROTEIN SUC2 FROM [ARABIDOPSIS THALIANA][PUTATIVE] | Transporter |
| 2090 | 313 | WALL-ASSOCIATED KINASE CONTAINS SIMILARITY TO SERINE/THREONINE KINASE GB Y12531 FROM BRASSICA OLERACEA[PUTATIVE] | Kinase, Protein |
| 2111 | 314 | PHOSPHOMETHYLPYRIMIDINE KINASE PROBABLE THIAMIN BIOSYNTHETIC ENZYME, LOCATION OF EST GB AA395737, GB T21651 | Kinase |
| 2119 | 315 | NADPH OXIDASE FLAVOCYTOCHROME SUPEROXIDE-GENERATING HIGHLY SIMILAR TO GB:CAA70769, FRO1 AND GB:CAA70770, FRO2 FROM [ARABIDOPSIS THALIANA][PUTATIVE] | Oxidase |
| 2125 | 316 | AUXIN TRANSPORT PROTEIN STRONGLY SIMILAR TO AUXIN TRANSPORT PROTEIN GB:AAD52697[PUTATIVE] | Transporter |
| 2137 | 317 | PECTINESTERASE SIMILAR TO GB:AAB57669, LOCATION OF EST GB Z35063 AND GB Z35062[PUTATIVE] | Esterase |
| 2154 | 318 | 2-HEXAPRENYL-1,4-NAPHTHOQUINONE METHYLTRANSFERASE GB:BAA25267 GI:2982680 FROM [MICROCOCCUS LUTEUS]SERINE O-ACETYLTRANSFERASE (EC 2.3.1.30) SAT-52 (PIR S71207) SPORE GERMINATION PROTEIN C2 SIMILAR TO | Transferases |
| 2164 | 319 | POLYGALACTURONASE, PUTATIVE SIMILAR TO POLYGALACTURONASE GB:BAA88472 GI:6624205 FROM [CUCUMIS SATIVUS] | Glycosylase |

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| 2165 | 320 | POLYGALACTURONASE PRECURSOR [PUTATIVE] | Glycosylase |
| 2166 | 321 | GLUCOSYLTRANSFERASE GB:AAD15455 GI:4263795 FROM [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN SIMILAR TO][PUTATIVE] | Transferases |
| 2187 | 322 | CARBONIC ANHYDRASE [PUTATIVE] | Anhydrase |
| 2212 | 323 | REVERSE TRANSCRIPTASE, PUTATIVE SIMILAR TO REVERSE TRANSCRIPTASE GB:BAA20419 GI:2193870 FROM [MUS MUSCULUS] | Transcriptase |
| 2220 | 324 | GLUCOSYLTRANSFERASE, PUTATIVE SIMILAR TO BETA-(1-3)-GLUCOSYL TRANSFERASE GB:AAC62210 GI:3687658 FROM [BRADYRHIZOBIUM JAPONICUM] | Transferases |
| 2222 | 325 | INDOLE-3-ACETATE BETA-GLUCOSYLTRANSFERASE SIMILAR TO GB:AAB64022[PUTATIVE] | Transferases |
| 2223 | 326 | PEROXIDASE SIMILAR TO PEROXIDASE ATP26A, GB:CAA72487[PUTATIVE] | Oxidase |
| 2229 | 327 | GLYCOSYL TRANSFERASE SIMILAR TO GB:AAC78704[PUTATIVE] | Transferases |
| 2246 | 328 | POLYKETIDE HYDROXYLASE FROM SEVERAL BACTERIAL SPECIES[HYPOTHETICAL PROTEIN SIMILAR TO] | Hydroxylase |
| 2252 | 329 | LYSINE/HISTIDINE-SPECIFIC PERMEASE SIMILAR TO GB:AAC49885, SIMILAR TO EST GB T13994[PUTATIVE] | Transporter |
| 2253 | 330 | DEACETYLVINDOLINE 4-O-ACETYLTRANSFERASE, GB:AAC9931; UNKNOWN PROTEIN SIMILAR TO | Transferases |
| 2254 | 331 | DEACETYLVINDOLINE 4-O-ACETYLTRANSFERASE, GB:AAC99311[HYPOTHETICAL PROTEIN SIMILAR TO] | Transferases |
| 2256 | 332 | RIBONUCLEASE III SIMILAR TO ESTS EMB Z18464 AND GB AA389811[PUTATIVE] | Nuclease |
| 2271 | 333 | PROTEIN KINASE SIMILAR TO GB:AAD21776, SIMILAR TO ESTS EMB Z18436, GB T21564, EMB F14127, AND GB T75836, DBJ D22341[PUTATIVE] | Kinase, Protein |
| 2273 | 334 | ANTHRANILATE SYNTHASE BETA SUBUNIT IDENTICAL TO ANTHRANILATE SYNTHASE BETA SUBUNIT GI:403434 FROM [ARABIDOPSIS THALIANA] | Synthase |

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| 2277 | 335 | ANTHRANILATE SYNTHASE BETA SUBUNIT IDENTICAL TO ANTHRANILATE SYNTHASE BETA SUBUNIT GI:403434 FROM [ARABIDOPSIS THALIANA] | Synthase |
| 2278 | 336 | PURPLE ACID PHOSPHATASE PRECURSOR GI:7331195 FROM [GLYCINE MAX][HYPOTHETICAL PROTEIN SIMILAR TO][PUTATIVE] | Phosphatase |
| 2294 | 337 | WALL-ASSOCIATED KINASE, PUTATIVE SIMILAR TO WALL-ASSOCIATED KINASE 1 GI:3549626 FROM [ARABIDOPSIS THALIANA] | Kinase, Protein |
| 2296 | 338 | TRNA ISOPENTENYL TRANSFERASE, PUTATIVE SIMILAR TO TRNA ISOPENTENYL TRANSFERASE GI:6006718 FROM [ARABIDOPSIS THALIANA] | Transferases |
| 2301 | 339 | DIHYDROFLAVONOL 4-REDUCTASE, PUTATIVE SIMILAR TO DIHYDROFLAVONOL 4-REDUCTASE GI:1332411 FROM [ROSA HYBRIDA] | Reductase |
| 2308 | 340 | LYSINE AND HISTIDINE SPECIFIC TRANSPORTER, PUTATIVE SIMILAR TO LYSINE AND HISTIDINE SPECIFIC TRANSPORTER GI:2576361 FROM [ARABIDOPSIS THALIANA] | Transporter |
| 2321 | 341 | ESTERASE 6 GI:606998 FROM [DROSOPHILA SIMULANS], HYPOTHETICAL PROTEIN CONTAINS SIMILARITY TO | Esterase |
| 2322 | 342 | P-TYPE TRANSPORTING ATPASE, PUTATIVE SIMILAR TO P-TYPE TRANSPORTING ATPASE GI:9229867 FROM [ARABIDOPSIS THALIANA] | Transporter |
| 2328 | 343 | URIDINE KINASE GI:6899310 FROM [UREAPLASMA UREALYTICUM][HYPOTHETICAL PROTEIN CONTAINS SIMILARITY TO] | Kinase |
| 2345 | 344 | ALPHA/BETA HYDROLASE GB:AAF67777 GI:7705098 FROM [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN SIMILAR TO][PUTATIVE] | Hydrolase |
| 2347 | 345 | RETICULINE OXIDASE-LIKE PROTEIN GB:CAB45850 GI:5262224 FROM [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN SIMILAR TO] | Oxidase |
| 2348 | 346 | RETICULINE OXIDASE-LIKE PROTEIN GB:CAB45850 GI:5262224 FROM [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN SIMILAR TO] | Oxidase |

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| 2349 | 347 | RETICULINE OXIDASE-LIKE PROTEIN GB:CAB45849 GI:5262223 FROM [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN SIMILAR TO] | Oxidase |
| 2350 | 348 | RETICULINE OXIDASE-LIKE PROTEIN GB:CAB45850 GI:5262224 FROM [ARABIDOPSIS THALIANA] UNKNOWN PROTEIN SIMILAR TO | Oxidase |
| 2351 | 349 | RETICULINE OXIDASE-LIKE PROTEIN GB:CAB45850 GI:5262224 FROM [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN SIMILAR TO] | Oxidase |
| 2352 | 350 | FATTY ACID ELONGASE 3-KETOACYL-COA SYNTHASE 1 SIMILAR TO PUTATIVE INTEGRAL MEMBRANE PROTEIN GB:AAD17424 GI:4335747 FROM [ARABIDOPSIS THALIANA] | Synthase |
| 2353 | 351 | BETA-1,3-GLUCANASE GB:AAD26909 GI:4662638 FROM [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN SIMILAR TO][PUTATIVE] | Glycosylase |
| 2389 | 352 | RIBONUCLEASE 3 PRECURSOR IDENTICAL TO SP:P42815 FROM [ARABIDOPSIS THALIANA] | Nuclease |
| 2393 | 353 | REVERSE TRANSCRIPTASE GB:AAD17398[HYPOTHETICAL PROTEIN SIMILAR TO] | Transcriptase |
| 2402 | 354 | REVERSE TRANSCRIPTASE GB:AAD22368[HYPOTHETICAL PROTEIN SIMILAR TO] | Transcriptase |
| 2409 | 355 | NITRATE TRANSPORTER, PUTATIVE NITRATE TRANSPORTER NTL1 GB:AAC28086 GI:3377517 FROM [ARABIDOPSIS THALIANA] | Transporter |
| 2417 | 356 | GALACTOSYLTRANSFERASE, UNKNOWN PROTEIN CONTAINS PFAM PROFILE:PF01762 | Transferases |
| 2418 | 357 | GLUTATHIONE TRANSFERASE, PUTATIVE SIMILAR TO GLUTATHIONE S-TRANSFERASE GB: AAF22517 GI:6652870 FROM [PAPAVER SOMNIFERUM] | Transferases |
| 2419 | 358 | GLUTATHIONE TRANSFERASE, PUTATIVE SIMILAR TO GLUTATHIONE S-TRANSFERASE GB: AAF22517 GI:6652870 FROM [PAPAVER SOMNIFERUM] | Transferases |
| 2421 | 359 | VALYL- TRNA SYNTHETASE, PUTATIVE SIMILAR TO VALYL-TRNA SYNTHETASE GB:P93736 GI:3122914 FROM [ARABIDOPSIS THALIANA] | Synthase |

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| 2424 | 360 | RECEPTOR KINASE, PUTATIVE SIMILAR TO CLV1 RECEPTOR KINASE GB:AAB58929 GI:2160756 FROM [ARABIDOPSIS THALIANA] | Kinase, Protein |
| 2437 | 361 | SENSORY TRANSDUCTION HISTIDINE KINASE SIMILAR TO GB:AAD21777; SIMILAR TO ESTS GB AA712891 AND GB AA042438[PUTATIVE] | Kinase, Protein |
| 2474 | 362 | LIPASE SIMILAR TO HYPOTHETICAL PROTEIN GB:AAF24946 GI:6693020 FROM [ARABIDOPSIS THALIANA][PUTATIVE] | Lipase |
| 2494 | 363 | POLYGALACTURONASE GB:AAC04907 GI:2924778 FROM [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN SIMILAR TO][PUTATIVE] | Glycosylase |
| 2510 | 364 | IRON/ASCORBATE OXIDOREDUCTASE FAMILY | Reductase |
| 2516 | 365 | POLY A POLYMERASE FAMILY MEMBERS[HYPOTHETICAL PROTEIN CONTAINS SIMILARITY TO] | Polymerase |
| 2525 | 366 | STEROID SULFOTRANSFERASE, PUTATIVE SIMILAR TO STEROID SULFOTRANSFERASE 3 GI:3420008 FROM [BRASSICA NAPUS] | Transferases |
| 2529 | 367 | PURINE PERMEASE, PUTATIVE SIMILAR TO PURINE PERMEASE GI:7620007 FROM [ARABIDOPSIS THALIANA] | Transporter |
| 2530 | 368 | PURINE PERMEASE IDENTICAL TO PURINE PERMEASE GI:7620007 FROM [ARABIDOPSIS THALIANA] | Transporter |
| 2542 | 369 | RECEPTOR KINASE, PUTATIVE SIMILAR TO RECEPTOR KINASE GI:4105699 FROM [ARABIDOPSIS THALIANA] | Kinase, Protein |
| 2547 | 370 | WALL-ASSOCIATED KINASE 1, PUTATIVE SIMILAR TO WALL-ASSOCIATED KINASE 1 GI:3549626 FROM [ARABIDOPSIS THALIANA] | Kinase, Protein |
| 2552 | 371 | RECEPTOR KINASE, PUTATIVE SIMILAR TO RECEPTOR KINASE GI:4105699 FROM [ARABIDOPSIS THALIANA] | Kinase, Protein |
| 2565 | 372 | LIPASE/HYDROLASE GDSL-LIKE MOTIF; PUTATIVE CONTAINS PFAM PROFILE: PF00657 LIPASE/ACYLHYDROLASE | Lipase |

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| 2566 | 373 | LIPASE/HYDROLASE GDSL-LIKE MOTIF; PUTATIVE CONTAINS PFAM PROFILE: PF00657 LIPASE/ACYLHYDROLASE | Lipase |
| 2567 | 374 | LIPASE/HYDROLASE GDSL-LIKE MOTIF; PUTATIVE CONTAINS PFAM PROFILE: PF00657 LIPASE/ACYLHYDROLASE | Lipase |
| 2568 | 375 | LIPASE/HYDROLASE GDSL-LIKE MOTIF; PUTATIVE CONTAINS PFAM PROFILE: PF00657 LIPASE/ACYLHYDROLASE | Lipase |
| 2569 | 376 | LIPASE/HYDROLASE GDSL-LIKE MOTIF; PUTATIVE CONTAINS PFAM PROFILE: PF00657 LIPASE/ACYLHYDROLASE | Lipase |
| 2571 | 377 | LIPASE, PUTATIVE SIMILAR TO LIPASE GB:AAA93262 GI:1145627 [ARABIDOPSIS THALIANA] | Lipase |
| 2572 | 378 | LIPASE/HYDROLASE GDSL-LIKE MOTIF; PUTATIVE CONTAINS PFAM PROFILE: PF00657 LIPASE/ACYLHYDROLASE | Lipase |
| 2574 | 379 | LIPASE IDENTICAL TO LIPASE GB:AAA93262 GI:1145627 [ARABIDOPSIS THALIANA] (FEBS LETT. 377 (3), 475-480 (1995)) | Lipase |
| 2575 | 380 | ANTHRANILATE HYDROXYCINNAMOYL/BENZOYLTRANSFERASE, PUTATIVE SIMILAR TO ANTHRANILATE N- HYDROXYCINNAMOYL/BENZOYLTRANSFERASE GB:Z84384 GI:2239084 [DIANTHUS CARYOPHYLLUS] | N-Transferases |
| 2617 | 381 | BETA-1,3 GLUCANASE, PUTATIVE SIMILAR TO GI:7414433 FROM [PISUM SATIVUM] | Glycosylase |
| 2620 | 382 | PHOSPHORIBOSYLANTHRANILATE ISOMERASE IDENTICAL TO GI:619749 FROM [ARABIDOPSIS THALIANA] (PLANT CELL 7 (4), 447-461 (1995)) | Isomerase |
| 2644 | 383 | REVERSE TRANSCRIPTASE, PUTATIVE SIMILAR TO GI:976278 FROM [ARABIDOPSIS THALIANA] | Transcriptase |
| 2645 | 384 | LIPASE/HYDROLASE GDSL-LIKE MOTIF; PUTATIVE CONTAINS PFAM PROFILE: PF00657 LIPASE/ACYLHYDROLASE | Lipase |

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| 2646 | 385 | LIPASE/HYDROLASE GDSL-LIKE MOTIF; PUTATIVE CONTAINS PFAM PROFILE: PF00657 LIPASE/ACYLHYDROLASE | Lipase |
| 2651 | 386 | RECEPTOR-LIKE SERINE/THREONINE KINASE (RFK1), PUTATIVE SIMILAR TO RECEPTOR-LIKE SERINE/THREONINE KINASE (RFK1) GI:9972369 FROM [ARABIDOPSIS THALIANA] | Kinase, Protein |
| 2652 | 387 | RECEPTOR-LIKE SERINE/THREONINE KINASE, PUTATIVE SIMILAR TO RECEPTOR-LIKE SERINE/THREONINE KINASE GI:2465923 FROM [ARABIDOPSIS THALIANA] | Kinase, Protein |
| 2653 | 388 | RECEPTOR PROTEIN KINASE, PUTATIVE SIMILAR TO RECEPTOR PROTEIN KINASE GI:1389566 FROM [ARABIDOPSIS THALIANA] | Kinase, Protein |
| 2654 | 389 | RECEPTOR-LIKE SERINE/THREONINE KINASE, PUTATIVE, 5' PARTIAL SIMILAR TO RECEPTOR-LIKE SERINE/THREONINE KINASE GI:2465923 FROM [ARABIDOPSIS THALIANA] | Kinase, Protein |
| 2660 | 390 | PHENYLALANINE HYDROXYLASE GI:476740 FROM [PSEUDOMONAS AERUGINOSA][HYPOTHETICAL PROTEIN CONTAINS SIMILARITY TO] | Hydroxylase |
| 2663 | 391 | ESTERASE GI:4191785 FROM [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN SIMILAR TO][PUTATIVE] | Esterase |
| 2686 | 392 | BETA-1,3-GLUCANASE PRECURSOR, PUTATIVE SIMILAR TO GI:4097948 FROM [ORYZA SATIVA] (GENE 223 (1-2), 311-320 (1998)) | Glycosylase |
| 2688 | 393 | 9-CIS-EPOXYCAROTENOID DIOXYGENASE, PUTATIVE SIMILAR TO 9-CIS-EPOXYCAROTENOID DIOXYGENASE GI:6715257 FROM [PHASEOLUS VULGARIS] | Oxygenases |
| 2689 | 394 | DIADENOSINE 5,5-P ₁ ,P ₄ -TETRAPHOSPHATE HYDROLASE, PUTATIVE SIMILAR TO DIADENOSINE 5,5-P ₁ ,P ₄ -TETRAPHOSPHATE HYDROLASE GI:1888556 FROM [LUPINUS ANGUSTIFOLIUS] | Hydrolase |
| 2705 | 395 | CYCLING-ASSOCIATED KINASE GI:1902912 FROM [RATTUS NORVEGICUS][HYPOTHETICAL PROTEIN CONTAINS SIMILARITY TO] | Kinase, Protein |

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| 2707 | 396 | HYDROLASE GI:7270684 FROM [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN SIMILAR TO][PUTATIVE] | Hydrolase |
| 2710 | 397 | PECTATE LYASE, PUTATIVE CONTAINS PFAM PROFILE: PF00544: PECTATE LYASE | Lyase |
| 2712 | 398 | LIPASE, PUTATIVE CONTAINS PFAM PROFILE: PF01764: LIPASE | Lipase |
| 2714 | 399 | REVERSE TRANSCRIPTASES, POSSIBLE PSEUDOGENE[HYPOTHETICAL PROTEIN SIMILAR TO], PORTIONS OF LINE-ELEMENT | Transcriptase |
| 2716 | 400 | ABC TRANSPORTER, PUTATIVE CONTAINS PFAM PROFILE: PF00005: ABC TRANSPORTER | Transporter |
| 2717 | 401 | ABC TRANSPORTER, PUTATIVE CONTAINS PFAM PROFILE: PF00005: ABC TRANSPORTER | Transporter |
| 2725 | 402 | FERRODOXIN NADP OXIDOREDUCTASE, PUTATIVE SIMILAR TO FERRODOXIN NADP OXIDOREDUCTASE GB:X99419 GI:1480346 FROM [PISUM SATIVUM] | Reductase |
| 2727 | 403 | UDP GLUCOSE:FLAVONOID 3-O-GLUCOSYLTRANSFERASE, PUTATIVE SIMILAR TO UDP GLUCOSE:FLAVONOID 3-O-GLUCOSYLTRANSFERASE GB:AAB81683 GI:2564114 FROM [VITIS VINIFERA] | Transferases |
| 2731 | 404 | SERINE/THREONINE PROTEIN KINASE CONTAINS EUKARYOTIC PROTEIN KINASE DOMAIN PF00069, SIMILAR TO GB:AAB47421[PUTATIVE] | Kinase, Protein |
| 2744 | 405 | RETICULINE OXIDASE-LIKE PROTEIN SIMILAR TO GB:P30986 FROM [ESCHSCHOLZIA CALIFORNICA] (BERBERINE BRIDGE-FORMING ENZYME), ESTS GB F19886, GB Z30784 AND GB Z30785 COME FROM THIS GENE[PUTATIVE] | Oxidase |
| 2745 | 406 | RETICULINE OXIDASE-LIKE PROTEIN SIMILAR TO GB:P30986 FROM [ESCHSCHOLZIA CALIFORNICA] (BERBERINE BRIDGE-FORMING ENZYME), ESTS GB F19886, GB Z30784 AND GB Z30785 COME FROM THIS GENE[PUTATIVE] | Oxidase |

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| 2746 | 407 | RETICULINE OXIDASE-LIKE PROTEIN SIMILAR TO GB:P30986 FROM [ESCHSCHOLZIA CALIFORNICA] (BERBERINE BRIDGE-FORMING ENZYME), ESTS GB F19886, GB Z30784 AND GB Z30785 COME FROM THIS GENE[PUTATIVE] | Oxidase |
| 2747 | 408 | RETICULINE OXIDASE-LIKE PROTEIN SIMILAR TO GB:P30986 FROM [ESCHSCHOLZIA CALIFORNICA] (BERBERINE BRIDGE-FORMING ENZYME), ESTS GB F19886, GB Z30784 AND GB Z30785 COME FROM THIS GENE[PUTATIVE] | Oxidase |
| 2748 | 409 | RETICULINE OXIDASE-LIKE PROTEIN SIMILAR TO GB:P30986 FROM [ESCHSCHOLZIA CALIFORNICA] (BERBERINE BRIDGE-FORMING ENZYME), ESTS GB F19886, GB Z30784 AND GB Z30785 COME FROM THIS GENE[PUTATIVE] | Oxidase |
| 2750 | 410 | RETICULINE OXIDASE-LIKE PROTEIN, 3' PARTIAL SIMILAR TO GB:P30986 FROM [ESCHSCHOLZIA CALIFORNICA] (BERBERINE BRIDGE-FORMING ENZYME), ESTS GB F19886, GB Z30784 AND GB Z30785 COME FROM THIS GENE[PUTATIVE] | Oxidase |
| 2759 | 411 | PEROXIDASE SIMILAR TO CATIONIC PEROXIDASE (GI 1232069); SIMILAR TO EST GB A1100412[PUTATIVE] | Oxidase |
| 2762 | 412 | VACUOLAR SORTING RECEPTOR SIMILAR TO (GI 3033390); SIMILAR TO EST DBJ C72582[PUTATIVE] | Receptor |
| 2784 | 413 | POTASSIUM TRANSPORTER SIMILAR TO POTASSIUM TRANSPORTER GB:AAB87687[PUTATIVE] | Transporter |
| 2794 | 414 | PHOSPHORIBOSYLGLYCINAMIDE FORMYLTRANSFERASE ALMOST IDENTICAL TO GB:P52422 FROM [ARABIDOPSIS THALIANA], INVOLVED WITH PURINE BIOSYNTHESIS[PUTATIVE] | Transferases |
| 2795 | 415 | ASPARTATE KINASE-HOMOSERINE DEHYDROGENASE ALMOST IDENTICAL TO GB X71364 GENE FOR ASPARTATE KINASE HOMOSERINE DEHYDROGENASE FROM ARABIDOPSIS THALIANA[PUTATIVE] | Dehydrogenases |

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| 2798 | 416 | IRON-REGULATED TRANSPORTER PROTEIN, PUTATIVE SIMILAR TO IRON-REGULATED TRANSPORTER 2 GB:AAD30549 GI:4836773 FROM [LYCOPERSICON ESCULENTUM] | Transporter |
| 2814 | 417 | PROTEIN KINASE, PUTATIVE CONTAINS PFAM PROFILE: PF00069: EUKARYOTIC PROTEIN KINASE DOMAIN | Kinase, Protein |
| 2821 | 418 | N-HYDROXYCINNAMOYL/BENZOYLTRANSFERASE, PUTATIVE SIMILAR TO N-HYDROXYCINNAMOYL/BENZOYLTRANSFERASE [IPOMOEA BATATAS] GI:6469032 | Transferases |
| 2836 | 419 | COPPER AMINE OXIDASE, PUTATIVE SIMILAR TO COPPER AMINE OXIDASE GI:4651202 FROM [PISUM SATIVUM] | Oxidase |
| 2838 | 420 | COPPER AMINE OXIDASE, PUTATIVE SIMILAR TO COPPER AMINE OXIDASE GI:685197 FROM [PISUM SATIVUM] | Oxidase |
| 2853 | 421 | AMINO ACID PERMEASE, PUTATIVE CONTAINS PFAM PROFILE: PF00324: AMINO ACID PERMEASE | Transporter |
| 2854 | 422 | AMINO ACID PERMEASE, PUTATIVE CONTAINS PFAM PROFILE: PF00324: AMINO ACID PERMEASE | Transporter |
| 2857 | 423 | PHOSPHORIBOSYL-ATP PYROPHOSPHOHYDROLASE (AT-IE) IDENTICAL TO PHOSPHORIBOSYL-ATP PYROPHOSPHOHYDROLASE (AT-IE) [ARABIDOPSIS THALIANA] GI:3461884 (PLANT PHYSIOL. 118 (1), 275-283 (1998)) | Hydrolase |
| 2859 | 424 | MAJOR INTRINSIC PROTEIN, PUTATIVE CONTAINS TIGRFAM PROFILE: TIGR00861: MIP FAMILY CHANNEL PROTEINS | Channel |
| 2860 | 425 | MAJOR INTRINSIC PROTEIN, PUTATIVE CONTAINS TIGRFAM PROFILE: TIGR00861: MIP FAMILY CHANNEL PROTEINS | Channel |
| 2865 | 426 | TERPENE SYNTHASE FAMILY PROTEIN, PUTATIVE CONTAINS PFAM PROFILE: PF01397: TERPENE SYNTHASE FAMILY | Synthase |

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| 2873 | 427 | SECRETORY CARRIER MEMBRANE PROTEIN, PUTATIVE SIMILAR TO SECRETORY CARRIER MEMBRANE PROTEIN GI:7109228 FROM [ARABIDOPSIS THALIANA] | Transporter |
| 2874 | 428 | PHOSPHORIBULOKINASE PRECURSOR IDENTICAL TO PHOSPHORIBULOKINASE PRECURSOR GB:P25697 GI:125576 FROM [ARABIDOPSIS THALIANA] | Kinase |
| 2878 | 429 | PINOESINOL-LARICIESINOL REDUCTASE, PUTATIVE SIMILAR TO PINOESINOL-LARICIESINOL REDUCTASE GB:AAF63508 GI:7542583 FROM [THUJA PLICATA] | Reductase |
| 2883 | 430 | OBTUSIFOLIOL 14-ALPHA-DEMETHYLASE (CYP51) GB:Y09292 GI:1707854 FROM [TRITICUM AESTIVUM], CONTAINS SIMILARITY TO | Methylase |
| 2884 | 431 | ENDOXYLOGLUCAN TRANSFERASE, PUTATIVE SIMILAR TO ENDOXYLOGLUCAN TRANSFERASE GB:AAD45125 GI:5533313 FROM [ARABIDOPSIS THALIANA] | Transferases |
| 2885 | 432 | CELLULOSE SYNTHASE CATALYTIC SUBUNIT, PUTATIVE SIMILAR TO CELLULOSE SYNTHASE CATALYTIC SUBUNIT GB:BAB09693 GI:9759258 FROM [ARABIDOPSIS THALIANA] | Synthase |
| 2887 | 433 | GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE IDENTICAL TO GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE GB:Q43307 FROM [ARABIDOPSIS THALIANA] | Transferases |
| 2897 | 434 | L-GULONOLACTONE OXIDASE GB:J03536 GI:204149 FROM [RATTUS NORVEGICUS] UNKNOWN PROTEIN CONTAINS SIMILARITY TO | Oxidase |
| 2898 | 435 | L-GULONOLACTONE OXIDASE GB:J03536 GI:204149 FROM [RATTUS NORVEGICUS] UNKNOWN PROTEIN CONTAINS SIMILARITY TO | Oxidase |
| 2902 | 436 | OXIDASE, PUTATIVE SIMILAR TO OXIDASE GB:AAA32870 GI:166876 FROM [ARABIDOPSIS THALIANA] | Oxidase |

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| 2930 | 437 | PROTEIN KINASE, PUTATIVE IDENTICAL TO BHLH PROTEIN GB:CAA67885 GI:1465368 FROM [ARABIDOPSIS THALIANA] | Kinase, Protein |
| 2938 | 438 | PROTEIN PHOSPHATASE 2C GB:CAA72341 GI:2582800 FROM [MEDICAGO SATIVA][HYPOTHETICAL PROTEIN CONTAINS SIMILARITY TO] | Phosphatase |
| 2952 | 439 | BETA-1,3-GLUCANASE PRECURSOR, PUTATIVE SIMILAR TO BETA-1,3-GLUCANASE PRECURSOR GI:4097948 FROM [ORYZA SATIVA] | Glycosylase |
| 2955 | 440 | STARCH SYNTHASE, PUTATIVE SIMILAR TO STARCH SYNTHASE GI:21613 FROM [SOLANUM TUBEROSUM] | Synthase |
| 2965 | 441 | NON-LTR RETROELEMENT REVERSE TRANSCRIPTASE[HYPOTHETICAL PROTEIN CONTAINS SIMILARITY TO][PUTATIVE] | Transcriptase |
| 2968 | 442 | CATECHOL O-METHYLTRANSFERASE, PUTATIVE SIMILAR TO CATECHOL O-METHYLTRANSFERASE GI:4808524 FROM [THALICTRUM TUBEROSUM] | Transferases |
| 2981 | 443 | BETA-1,3-GLUCANASE, PUTATIVE SIMILAR TO ENDO- 1,3-BETA-GLUCANASE GB:AAC39322 GI:2735502 FROM [HORDEUM VULGARE] | Glycosylase |
| 2985 | 444 | PROTEIN KINASE, PUTATIVE CONTAINS PFAM PROFILE: PF00069: EUKARYOTIC PROTEIN KINASE DOMAIN | Kinase, Protein |
| 2999 | 445 | NITRATE TRANSPORTER NTL1, PUTATIVE SIMILAR TO GI:3377517 FROM [ARABIDOPSIS THALIANA] | Transporter |
| 3015 | 446 | EPIDERMAL GROWTH FACTOR RECEPTOR-LIKE PROTEIN GB:AAB31972 GI:9256501 FROM [XIPHOPHORUS MACULATUS][HYPOTHETICAL PROTEIN CONTAINS SIMILARITY TO] | Receptor |
| 3017 | 447 | DISEASE RESISTANCE PROTEIN, PUTATIVE SIMILAR TO RECEPTOR KINASE-LIKE PROTEIN GB:AAB82755 GI:2586083 FROM [ORYZA LONGISTAMINATA] (SCIENCE 270 (5243), 1804-1806 (1995)) | Kinase, Protein |
| 3024 | 448 | TERPENE SYNTHASE, PUTATIVE SIMILAR TO DELTA- CADINENE SYNTHASE ISOZYME A GB:Q43714 FROM [GOSSYPIUM ARBOREUM] | Synthase |

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| 3050 | 449 | POLYNEURIDINE ALDEHYDE ESTERASE, PUTATIVE SIMILAR TO POLYNEURIDINE ALDEHYDE ESTERASE GI:6651393 FROM [RAUVOLFIA SERPENTINA] | Esterase |
| 3062 | 450 | RECEPTOR PROTEIN KINASE-LIKE PROTEIN GI:10177178 FROM [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN CONTAINS SIMILARITY TO] | Kinase, Protein |
| 3066 | 451 | PSEUDOURIDINE SYNTHASES[PUTATIVE], PROTEIN CONTAINS SIMILARITY TO | Synthase |
| 3072 | 452 | SOMATIC EMBRYOGENESIS RECEPTOR-LIKE KINASE, PUTATIVE SIMILAR TO SOMATIC EMBRYOGENESIS RECEPTOR-LIKE KINASE GI:2224910 FROM [DAUCUS CAROTA] | Kinase, Protein |
| 3079 | 453 | RECEPTOR-LIKE PROTEIN KINASE GI:6979335 FROM [ORYZA SATIVA][HYPOTHETICAL PROTEIN CONTAINS SIMILARITY TO] | Kinase, Protein |
| 3082 | 454 | PEROXIDASE, PUTATIVE SIMILAR TO GI:1199777 FROM [POPULUS NIGRA] | Oxidase |
| 3087 | 455 | DNA POLYMERASE I, PUTATIVE SIMILAR TO GI:4090935 FROM [RHODOTHERMUS SP. 'ITI 518'] | Polymerase |
| 3091 | 456 | PROTEIN KINASE DOMAIN (2 COPIES), PF00560 LEUCINE RICH REPEAT (17 COPIES) | Kinase, Protein |
| 3099 | 457 | PEROXIDASE ATP13A, PUTATIVE SIMILAR TO GB:CAA67312 FROM [ARABIDOPSIS THALIANA] | Oxidase |
| 3121 | 458 | PROTEIN PHOSPHATASE TYPE 2C, PUTATIVE SIMILAR TO GB:AAD17805 FROM [LOTUS JAPONICUS] (PROC. NATL. ACAD. SCI. U.S.A. 96 (4), 1738-1743 (1999)) | Phosphatase |
| 3143 | 459 | HYOSCYAMINE 6-DIOXYGENASE HYDROXYLASE, PUTATIVE SIMILAR TO HYOSCYAMINE 6- DIOXYGENASE HYDROXYLASE GB:P24397 FROM [HYOSCYAMUS NIGER] | Oxygenases |
| 3199 | 460 | PROTEIN KINASE, PUTATIVE SIMILAR TO MANY PREDICTED PROTEIN KINASES | Kinase, Protein |
| 3214 | 461 | TREHALOSE-PHOSPHATASE, PUTATIVE CONTAINS TIGRFAM PROFILE: TIGR00685: TREHALOSE- PHOSPHATASE | Phosphatase |

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| 3239 | 462 | ACETYL-COA CARBOXYLASE, PUTATIVE SIMILAR TO GI:1100253 FROM [ARABIDOPSIS THALIANA] | Carboxylase |
| 3244 | 463 | ADENYLOSUCCINATE LYASE-LIKE PROTEIN SIMILAR TO SP:P44797 FROM [HAEMOPHILUS INFLUENZAE] | Lyase |
| 3249 | 464 | VANILLOID RECEPTOR-LIKE PROTEIN GB:AAD26363 FROM [HOMO SAPIENS][HYPOTHETICAL PROTEIN SIMILAR TO] | Receptor |
| 3284 | 465 | NON-LTR REVERSE TRANSCRIPTASES[HYPOTHETICAL PROTEIN CONTAINS SIMILARITY TO] | Transcriptase |
| 3290 | 466 | BIOTIN HOLOCARBOXYLASE SYNTHETASE, PUTATIVE SIMILAR TO BIOTIN HOLOCARBOXYLASE SYNTHETASE GI:4874309 FROM [ARABIDOPSIS THALIANA] | Synthase |
| 3340 | 467 | PECTINESTERASE, PUTATIVE, 5' PARTIAL SIMILAR TO GI:1944574 FROM [LYCOPERSICON ESCULENTUM] | Esterase |
| 3394 | 468 | POLYGALACTURONASE, PUTATIVE SIMILAR TO POLYGALACTURONASE GI:288611 FROM [ZEA MAYS] | Glycosylase |
| 3395 | 469 | POLYGALACTURONASE, PUTATIVE SIMILAR TO POLYGALACTURONASE GI:288611 FROM [ZEA MAYS] | Glycosylase |
| 3396 | 470 | POLYGALACTURONASE, PUTATIVE SIMILAR TO POLYGALACTURONASE GI:288611 FROM [ZEA MAYS] | Glycosylase |
| 3413 | 471 | NON-LTR RETROELEMENT REVERSE TRANSCRIPTASE GI:4006833 FROM [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN SIMILAR TO][PUTATIVE] | Transcriptase |
| 3418 | 472 | STEROL GLUCOSYLTRANSFERASE, PUTATIVE SIMILAR TO STEROL GLUCOSYLTRANSFERASE GI:4731867 FROM [DICTYOSTELIUM DISCOIDEUM] | Transferases |
| 3427 | 473 | HISTIDINE DECARBOXYLASE, PUTATIVE SIMILAR TO HISTIDINE DECARBOXYLASE GB:BAA78331 GI:4996105 FROM [BRASSICA NAPUS] | Decarboxylase |
| 3435 | 474 | REVERSE TRANSCRIPTASE, PUTATIVE SIMILAR TO REVERSE TRANSCRIPTASE GB:CAA73798 GI:2462134 FROM [BETA VULGARIS] | Transcriptase |

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| 3439 | 475 | STEAROYL ACYL CARRIER PROTEIN DESATURASE, PUTATIVE SIMILAR TO STEAROYL ACYL CARRIER PROTEIN DESATURASE LLDD3A20 GB: AAD28287 GI:4704824 FROM [LUPINUS LUTEUS] | Desaturases |
| 3455 | 476 | NON-LTR RETROELEMENT REVERSE TRANSCRIPTASE GI:4544460 FROM [ARABIDOPSIS THALIANA], UNKNOWN PROTEIN SIMILAR TO PUTATIVE | Transcriptase |
| 3464 | 477 | GIBBERELLIN 20-OXIDASE, PUTATIVE, 5' PARTIAL SIMILAR TO GIBBERELIN 20-OXIDASE GI:4164141 FROM [LACTUCA SATIVA] | Oxidase |
| 3470 | 478 | AMINO ACID PERMEASE, PUTATIVE ALMOST IDENTICAL TO AMINO ACID PERMEASE GI:608673 FROM [ARABIDOPSIS THALIANA] | Transporter |
| 3471 | 479 | GIBBERELLIN 20-OXIDASE, PUTATIVE SIMILAR TO GIBBERELIN 20-OXIDASE GI:4164141 FROM [LACTUCA SATIVA] | Oxidase |
| 3497 | 480 | PEROXIDASE ATP18A, 3' PARTIAL IDENTICAL TO GB:CAA67336 FROM [ARABIDOPSIS THALIANA] | Oxidase |
| 3498 | 481 | PECTIN METHYLESTERASE, PUTATIVE SIMILAR TO PECTIN METHYLESTERASE GI:1617588 FROM [LYCOPERSICON ESCULENTUM] | Esterase |
| 3537 | 482 | NON-LTR RETROELEMENT REVERSE TRANSCRIPTASE GI:3746069 FROM [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN SIMILAR TO][PUTATIVE] | Transcriptase |
| 3544 | 483 | PHYTOCHELATIN SYNTHETASE GI:3559805 FROM [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN SIMILAR TO][PUTATIVE] | Synthase |
| 3545 | 484 | AAA-TYPE ATPASE-LIKE PROTEIN GI:9759053 FROM [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN SIMILAR TO] | ATPase |
| 3564 | 485 | NON-LTR RETROELEMENT REVERSE TRANSCRIPTASE GB:AAD21515 GI:4510429 FROM [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN SIMILAR TO][PUTATIVE] | Transcriptase |
| 3570 | 486 | PROTEIN PHOSPHATASE 2C GB:AAD25933 GI:4587992 FROM [ARABIDOPSIS THALIANA] | Phosphatase |

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| 3578 | 487 | ESTERASE GI:4335745 FROM [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN SIMILAR TO][PUTATIVE] | Esterase |
| 3597 | 488 | LYSINE AND HISTIDINE SPECIFIC TRANSPORTER, PUTATIVE SIMILAR TO LYSINE AND HISTIDINE SPECIFIC TRANSPORTER GI:2576361 FROM [ARABIDOPSIS THALIANA] | Transporter |
| 3610 | 489 | NON-LTR RETROELEMENT REVERSE TRANSCRIPTASE GB:AAC63678 GI:3738337 FROM [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN SIMILAR TO][PUTATIVE] | Transcriptase |
| 3632 | 490 | DIOXYGENASE, PUTATIVE SIMILAR TO DIOXYGENASE GB:CAA70330 GI:1666096 FROM [MARAH MACROCARPUS] | Oxygenases |
| 3643 | 491 | POLYGALACTURONASE PG1, PUTATIVE SIMILAR TO GB:AAD46483 FROM [GLYCINE MAX] (MOL. PLANT MICROBE INTERACT. 12 (6), 490-498 (1999)) | Glycosylase |
| 3660 | 492 | G PROTEIN COUPLED RECEPTOR IDENTICAL TO PUTATIVE G PROTEIN COUPLED RECEPTOR GI:2104224 FROM [ARABIDOPSIS THALIANA][PUTATIVE] | Receptor |
| 3674 | 493 | 1-AMINOCYCLOPROPANE-1-CARBOXYLATE DEAMINASE [UNKNOWN PROTEIN CONTAINS SIMILARITY TO] | Deaminase |
| 3680 | 494 | PROTEIN KINASE, PUTATIVE CONTAINS SIMILARITY TO MANY PREDICTED PROTEIN KINASES | Kinase, Protein |
| 3696 | 495 | LYSINE AND HISTIDINE SPECIFIC TRANSPORTER, PUTATIVE SIMILAR TO LYSINE AND HISTIDINE SPECIFIC TRANSPORTER GI:2576361 FROM [ARABIDOPSIS THALIANA] | Transporter |
| 3703 | 496 | LECTIN RECEPTOR KINASE, PUTATIVE SIMILAR TO LECTIN RECEPTOR KINASE GI:1769897 FROM [ARABIDOPSIS THALIANA] | Kinase, Protein |
| 3711 | 497 | TERPENE CYCLASE, PUTATIVE SIMILAR TO TERPENE CYCLASE GI:9293912 FROM [ARABIDOPSIS THALIANA] | Cyclase |
| 3712 | 498 | TERPENE CYCLASE, PUTATIVE SIMILAR TO TERPENE CYCLASE GI:9293912 FROM [ARABIDOPSIS THALIANA] | Cyclase |

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| 3715 | 499 | CHORISMATE SYNTHASE, PUTATIVE SIMILAR TO CHORISMATE SYNTHASE GI:452796 FROM [SYNECHOCYSTIS SP.]. | Synthase |
| 3720 | 500 | FLAVIN-CONTAINING MONOOXYGENASE, PUTATIVE SIMILAR TO FLAVIN-CONTAINING MONOOXYGENASE 4 GI:31429 FROM [HOMO SAPIENS] | Oxygenases |
| 3736 | 501 | LIGHT REPRESSIBLE RECEPTOR PROTEIN KINASE, PUTATIVE SIMILAR TO LIGHT REPRESSIBLE RECEPTOR PROTEIN KINASE GI:1321686 FROM [ARABIDOPSIS THALIANA] | Kinase, Protein |
| 3753 | 502 | RECEPTOR-LIKE KINASE GI:2224910 FROM [DAUCUS CAROTA][HYPOTHETICAL PROTEIN CONTAINS SIMILARITY TO] | Kinase, Protein |
| 3764 | 503 | FLAVONOL SYNTHASE, PUTATIVE SIMILAR TO FLAVONOL SYNTHASE GI:311657 FROM [PETUNIA HYBRIDA] | Synthase |
| 3776 | 504 | GERANYL GERANYL PYROPHOSPHATE SYNTHASE, PUTATIVE SIMILAR TO GERANYL GERANYL PYROPHOSPHATE SYNTHASE GB:BAA23157 GI:2578822 FROM [ARABIDOPSIS THALIANA] | Synthase |
| 3780 | 505 | PEROXIDASE, PUTATIVE SIMILAR TO PEROXIDASE GB:P80679 FROM [ARMORACIA RUSTICANA] | Oxidase |
| 3787 | 506 | ESTERASE GB:AAD17422 GI:4335745 FROM [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN SIMILAR TO][PUTATIVE] | Esterase |
| 3788 | 507 | ESTERASE GB:AAD17422 GI:4335745 FROM [ARABIDOPSIS THALIANA; UNKNOWN PROTEIN SIMILAR TO] | Esterase |
| 3789 | 508 | ESTERASE GB:AAD17422 GI:4335745 FROM [ARABIDOPSIS THALIANA]ESTERASE GB:AAD17422 GI:4335745 FROM [ARABIDOPSIS THALIANA; UNKNOWN PROTEIN SIMILAR TO UNKNOWN PROTEIN SIMILAR TO] | Esterase |
| 3793 | 509 | FUCOSYLTRANSFERASE C3 PROTEIN, PUTATIVE SIMILAR TO FUCOSYLTRANSFERASE C3 PROTEIN GB:CAB52254 GI:5702039 FROM [VIGNA RADIATA] | Transferases |

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| 3796 | 510 | MAP3K-LIKE PROTEIN KINASE GB:CAB16796 GI:4006878 FROM [ARABIDOPSIS THALIANA] | Kinase, Protein |
| 3801 | 511 | GLUTAMINE AMIDOTRANSFERASES CLASS-II GLUTAMINE AMIDOTRANSFERASE CLASS-I HISTONE ACETYLTRANSFERASE HAT B HYPOTHETICAL PROTEIN CONTAINS PFAM PROFILE: PF00117 HYPOTHETICAL PROTEIN CONTAINS PFAM PROFILE: PF00310 | Transferases |
| 3803 | 512 | NA ⁺ /H ⁺ ANTIporter, PUTATIVE SIMILAR TO PROTEIN CONTAINED WITHIN GB:AE001273 FROM [CHLAMYDIA TRACHOMATIS] | Transporter |
| 3808 | 513 | GLUTATHIONE S-TRANSFERASE, PUTATIVE SIMILAR TO GI:860955 FROM [HYOSCYAMUS MUTICUS] (PLANT PHYSIOL. 109 (1), 253-260 (1995)) | Transferases |
| 3825 | 514 | PHOSPHATIDYLINOSITOL 3-KINASE TORI GB:AAD16273 GI:4323240 FROM [FILOBASIDIELLA NEOFORMANS], UNKNOWN PROTEIN CONTAINS SIMILARITY TO | Kinase |
| 3828 | 515 | BRANCHED-CHAIN AMINO ACID AMINOTRANSFERASE, PUTATIVE SIMILAR TO BRANCHED-CHAIN AMINO ACID AMINOTRANSFERASE GB:AAF07191 GI:6319165 FROM [SOLANUM TUBEROSUM] | Transferases |
| 3835 | 516 | NON-LTR RETROELEMENT REVERSE TRANSCRIPTASE GB:AAD25836 GI:4587608 FROM [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN SIMILAR TO][PUTATIVE] | Transcriptase |
| 3856 | 517 | FRUCTOKINASE, PUTATIVE SIMILAR TO FRUCTOKINASE GB:U37838 GI:1052972 FROM [BETA VULGARIS] | Kinase |
| 3873 | 518 | UDP RHAMNOSE: ANTHOCYANIDIN-3-GLUCOSIDE RHAMNOSYLTRANSFERASE, PUTATIVE SIMILAR TO UDP RHAMNOSE: ANTHOCYANIDIN-3-GLUCOSIDE RHAMNOSYLTRANSFERASE [PETUNIA X HYBRIDA] GI:397567 | Transferases |

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| 3876 | 519 | PROTEIN KINASE, PUTATIVE CONTAINS PFAM PROFILE: PF00069: EUKARYOTIC PROTEIN KINASE DOMAIN | Kinase, Protein |
| 3898 | 520 | DNA POLYMERASE A FAMILY PROTEIN, PUTATIVE CONTAINS PFAM. PROFILE: PF00476: DNA POLYMERASE FAMILY A | Polymerase |
| 3909 | 521 | GIBBERELLIN 20-OXIDASE, PUTATIVE SIMILAR TO GIBBERELLIN 20-OXIDASE [TRITICUM AESTIVUM] GI:2222796 | Oxidase |
| 3912 | 522 | PROTEIN KINASE, PUTATIVE CONTAINS PFAM PROFILE: PF00069: EUKARYOTIC PROTEIN KINASE DOMAIN | Kinase, Protein |
| 3919 | 523 | DNA POLYMERASE III, EPSILON SUBUNIT GI:8163241 FROM [CHLAMYDIA MURIDARUM][HYPOTHETICAL PROTEIN CONTAINS SIMILARITY TO] | Polymerase |
| 3923 | 524 | ANTHRANILATE SYNTHASE LARGE SUBUNIT GI:1374671 FROM [BUCHNERA APHIDICOLA], UNKNOWN PROTEIN CONTAINS SIMILARITY TO | Synthase |
| 3932 | 525 | GLUCOSYL TRANSFERASE [PUTATIVE] | Transferases |
| 3952 | 526 | CINNAMYL ALCOHOL DEHYDROGENASE, PUTATIVE SIMILAR TO GB:X88797 FROM [EUCALYPTUS GUNNII] (PLANT MOL. BIOL. 36 (5), 755-765 (1998)) | Dehydrogenases |
| 3968 | 527 | ANTHRANILATE PHOSPHORIBOSYLTRANSFERASE, PUTATIVE SIMILAR TO PIR:T06460 FROM [PISUM SATIVUM] | Transferases |
| 3983 | 528 | NADP-SPECIFIC GLUTATAMATE DEHYDROGENASE, PUTATIVE SIMILAR TO NADP-SPECIFIC GLUTATAMATE DEHYDROGENASE (NADP-GDH) SP:P28724 [GIARDIA LAMBLIA (GIARDIA INTESTINALIS)] | Dehydrogenase |
| 3986 | 529 | REVERSE TRANSCRIPTASES[HYPOTHETICAL PROTEIN SIMILAR TO] | Transcriptase |
| 3987 | 530 | IAA-ALA HYDROLASE (IAR3) IDENTICAL TO IAA-ALA HYDROLASE (IAR3) [ARABIDOPSIS THALIANA] GI:3421384 | Hydrolase |

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| 3989 | 531 | AUXIN CONJUGATE HYDROLASE (ILL5) IDENTICAL TO AUXIN CONJUGATE HYDROLASE [ARABIDOPSIS THALIANA] (ILL5) GI:5725649;CONTAINS NONCONSENSUS AT ACCEPTOR SPLICE SITE AT EXON3 | Hydrolase |
| 3990 | 532 | RECEPTOR PROTEIN KINASE, PUTATIVE CONTAINS PFAM PROFILES: PF00069: EUKARYOTIC PROTEIN KINASE DOMAIN, MULTIPLE PF00560: LEUCINE RICH REPEAT | Kinase, Protein |
| 3991 | 533 | RECEPTOR PROTEIN KINASE, PUTATIVE CONTAINS PFAM PROFILES: PF00069: EUKARYOTIC PROTEIN KINASE DOMAIN, MULTIPLE PF00560: LEUCINE RICH REPEAT | Kinase, Protein |
| 3992 | 534 | RECEPTOR PROTEIN KINASE, PUTATIVE CONTAINS PFAM PROFILES: PF00069: EUKARYOTIC PROTEIN KINASE DOMAIN, MULTIPLE PF00560: LEUCINE RICH REPEAT | Kinase, Protein |
| 3996 | 535 | LIGHT REPRESSIBLE RECEPTOR PROTEIN KINASE, PUTATIVE SIMILAR TO LIGHT REPRESSIBLE RECEPTOR PROTEIN KINASE GI:1321686 FROM [ARABIDOPSIS THALIANA] | Kinase, Protein |
| 4001 | 536 | LIGHT REPRESSIBLE RECEPTOR PROTEIN KINASE, PUTATIVE SIMILAR TO LIGHT REPRESSIBLE RECEPTOR PROTEIN KINASE GI:1321686 FROM [ARABIDOPSIS THALIANA] | Kinase, Protein |
| 4011 | 537 | CAFFEIC ACID O-METHYLTRANSFERASE, PUTATIVE SIMILAR TO CAFFEIC ACID O-METHYLTRANSFERASE GI:5031492 FROM [OCIMUM BASILICUM] | Transferases |
| 4039 | 538 | PROTEIN KINASE, PUTATIVE SIMILAR TO GI:7573596 FROM [POPULUS NIGRA] | Kinase, Protein |
| 4041 | 539 | PROTEIN KINASE, PUTATIVE SIMILAR TO GI:7573596 FROM [POPULUS NIGRA] | Kinase, Protein |
| 4044 | 540 | SHORT CHAIN ALCOHOL DEHYDROGENASE, PUTATIVE SIMILAR TO GI:2739279 FROM [NICOTIANA TABACUM] (PLANT MOL. BIOL. 29 (5), 1027-1038 (1995)) | Dehydrogenase |

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| 4051 | 541 | GLYCOSYL TRANSFERASE, PUTATIVE SIMILAR TO PFAM PROFILE: PF00534 GLYCOSYL TRANSFERASES GROUP 1 | Transferases |
| 4053 | 542 | GLYCOSYL TRANSFERASES-LIKE PROTEIN GI:9294599 FROM [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN SIMILAR TO] | Transferases |
| 4065 | 543 | SOMATIC EMBRYOGENESIS RECEPTOR-LIKE KINASE, PUTATIVE SIMILAR TO SOMATIC EMBRYOGENESIS RECEPTOR-LIKE KINASE GI:2224910 FROM [DAUCUS CAROTA] | Kinase, Protein |
| 4081 | 544 | LYSOPHOSPHOLIPASE GI:1552244 FROM [RATTUS NORVEGICUS]; UNKNOWN PROTEIN CONTAINS SIMILARITY TO | Lipase |
| 4086 | 545 | AB HYDROLASE DOMAIN | Hydrolase |
| 4087 | 546 | LIPASE SIMILAR TO MONOGLYCERIDE LIPASE GB:NP_035974 FROM [MUS MUSCULUS][PUTATIVE] | Lipase |
| 4090 | 547 | OXYGENASE OXIDOREDUCTASE SIMILAR TO ADVENTITIOUS ROOTING RELATED GB:CAA12386 FROM [MALUS DOMESTICA][PUTATIVE] | Reductase |
| 4091 | 548 | GIBBERELLIN 20-OXIDASE GB:1581592 FROM [ARABIDOPSIS THALIANA][PUTATIVE], OXIDOREDUCTASE SIMILAR TO | Oxidase |
| 4092 | 549 | OXYGENASE OXIDOREDUCTASE SIMILAR TO ADVENTITIOUS ROOTING RELATED GB:CAA12386 FROM [MALUS DOMESTICA][PUTATIVE] | Reductase |
| 4093 | 550 | GIBBERELLIN 20-OXIDASE GB:AAD42693 FROM [CITRULLUS LANATUS][PUTATIVE], OXIDOREDUCTASE SIMILAR TO | Oxidase |
| 4104 | 551 | PURPLE ACID PHOSPHATASE SIMILAR TO PURPLE ACID PHOSPHATASE GB:CAA06921 FROM [IPOMOEA BATATAS][PUTATIVE] | Phosphatase |
| 4110 | 552 | DEOXYOCTULONOSIC ACID SYNTHETASE SIMILAR TO 3-DEOXY-MANNO-OCTULOSONATE CYTIDYLYLTRANSFERASE GB:P04951 FROM [ESCHERICHIA COLI][PUTATIVE] | Synthase |

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| 4117 | 553 | PROTEIN KINASE, PUTATIVE SIMILAR TO MANY PREDICTED PROTEIN KINASES | Kinase, Protein |
| 4118 | 554 | PROTEIN KINASE, PUTATIVE SIMILAR TO MANY PREDICTED PROTEIN KINASES | Kinase, Protein |
| 4119 | 555 | PROTEIN KINASE, PUTATIVE SIMILAR TO MANY PREDICTED PROTEIN KINASES | Kinase, Protein |
| 4143 | 556 | PHOSPHOENOLPYRUVATE CARBOXYLASE 1, PUTATIVE SIMILAR TO PHOSPHOENOLPYRUVATE CARBOXYLASE 1 GI:2266947 FROM [GOSSYPIMUM HIRSUTUM] | Carboxylase |
| 4154 | 557 | RECEPTOR-LIKE SERINE/THREONINE KINASE, PUTATIVE SIMILAR TO RECEPTOR-LIKE SERINE/THREONINE KINASE GB:AAC50043 GI:2465923 FROM [ARABIDOPSIS THALIANA] | Kinase, Protein |
| 4155 | 558 | RECEPTOR-LIKE SERINE/THREONINE KINASE, PUTATIVE SIMILAR TO RECEPTOR-LIKE SERINE/THREONINE KINASE GB:AAC50043 GI:2465923 FROM [ARABIDOPSIS THALIANA] | Kinase, Protein |
| 4163 | 559 | CHALCONE ISOMERASE, PUTATIVE SIMILAR TO GI:4126399 FROM [CITRUS SINENSIS] | Isomerase |
| 4178 | 560 | GLUTATHIONE TRANSFERASE, PUTATIVE SIMILAR TO GI:2853219 FROM [CARICA PAPAYA] | Transferases |
| 4183 | 561 | LEUCINE-RICH REPEAT TRANSMEMBRANE PROTEIN KINASE 1, PUTATIVE SIMILAR TO GI:3360289 FROM [ZEA MAYS] (PLANT MOL. BIOL. 37 (5), 749-761 (1998)) | Kinase, Protein |
| 4184 | 562 | LEUCINE-RICH REPEAT TRANSMEMBRANE PROTEIN KINASE 1, PUTATIVE SIMILAR TO GI:3360289 FROM [ZEA MAYS] (PLANT MOL. BIOL. 37 (5), 749-761 (1998)) | Kinase, Protein |
| 4193 | 563 | PECTIN METHYLESTERASE (PMEU1), PUTATIVE SIMILAR TO PECTIN METHYLESTERASE (PMEU1) GI:1222551 FROM [LYCOPERSICON ESCULENTUM] | Esterase |
| 4194 | 564 | PECTINESTERASE, PUTATIVE SIMILAR TO PECTINESTERASE GI:732912 FROM [PHASEOLUS VULGARIS] | Esterase |

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| 4202 | 565 | LIPASE/HYDROLASE GDSL-like motif PROTEIN GI:9759145 FROM [ARABIDOPSIS THALIANA], UNKNOWN PROTEIN SIMILAR TO | Lipase |
| 4203 | 566 | LIPASE, PUTATIVE SIMILAR TO LIPASE GI:1145627 FROM [ARABIDOPSIS THALIANA] | Lipase |
| 4208 | 567 | LIPASE, PUTATIVE SIMILAR TO LIPASE GI:1145627 FROM [ARABIDOPSIS THALIANA] | Lipase |
| 4278 | 568 | NADH DEHYDROGENASE SUBUNIT 3 GI:7542364 FROM [PAGURUS LONGICARPUS][HYPOTHETICAL PROTEIN CONTAINS SIMILARITY TO] | Dehydrogenase |
| 4286 | 569 | PROTEIN KINASE, PUTATIVE SIMILAR TO PROTEIN KINASE GI:9294282 FROM [ARABIDOPSIS THALIANA] | Kinase, Protein |
| 4298 | 570 | GLYCOSYL TRANSFERASE GI:7021339 FROM [SINORHIZOBIUM MELILOTI][HYPOTHETICAL PROTEIN CONTAINS SIMILARITY TO] | Transferases |
| 4299 | 571 | NADH DEHYDROGENASE SUBUNIT 6 GI:2660574 FROM [FICEDULA HYPOLEUCA][HYPOTHETICAL PROTEIN CONTAINS SIMILARITY TO] | Dehydrogenase |
| 4300 | 572 | NON-LTR RETROELEMENT REVERSE TRANSCRIPTASE GI:3785984 FROM [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN SIMILAR TO][PUTATIVE] | Transcriptase |
| 4315 | 573 | BETA-FRUCTOFURANOSIDASE, PUTATIVE SIMILAR TO BETA-FRUCTOFURANOSIDASE GI:9294027 FROM [ARABIDOPSIS THALIANA] | Glycosylase |
| 4323 | 574 | PROTEIN KINASE, PUTATIVE CONTAINS PFAM PROFILE: PF00069 EUKARYOTIC PROTEIN KINASE DOMAIN | Kinase, Protein |
| 4332 | 575 | LEUCOANTHOCYANIDIN DIOXYGENASE 2, PUTATIVE SIMILAR TO GI:5924383 FROM [DAUCUS CAROTA] | Oxygenases |
| 4351 | 576 | TYROSINE PHOSPHATASE GB:AAF81798 GI:8926334 FROM [ORYZA SATIVA], SIMILAR TO PUTATIVE | Phosphatase |
| 4364 | 577 | RECEPTOR KINASE, PUTATIVE SIMILAR TO CLV1 RECEPTOR KINASE GB:AAB58929 GI:2160756 FROM [ARABIDOPSIS THALIANA] | Kinase, Protein |

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| 4375 | 578 | H ⁺ /CA ²⁺ ANTIporter, PUTATIVE SIMILAR TO H ⁺ /CA ²⁺ EXCHANGER 2 GB:BAA75232 GI:4512263 FROM [IPOMOEA NIL] | Transporter |
| 4376 | 579 | H ⁺ /CA ²⁺ ANTIporter, PUTATIVE SIMILAR TO H ⁺ /CA ²⁺ EXCHANGER 2 GB:BAA75232 GI:4512263 FROM [IPOMOEA NIL] | Transporter |
| 4389 | 580 | CELLULOSE SYNTHASE CATALYTIC SUBUNIT, PUTATIVE SIMILAR TO GB:AAD39534 FROM [GOSSYPIMUM HIRSUTUM] | Synthase |
| 4396 | 581 | SERINE ACETYLTRANSFERASE IDENTICAL TO GB:CAA84371 FROM [ARABIDOPSIS THALIANA] (EUR. J. BIOCHEM. 227 (1-2), 500-509 (1995)) | Transferases |
| 4417 | 582 | WALL-ASSOCIATED KINASE 2, PUTATIVE SIMILAR TO RECEPTOR-LIKE SERINE/THREONINE KINASE GB:AAC50043 GI:2465923 FROM [ARABIDOPSIS THALIANA] | Kinase, Protein |
| 4418 | 583 | RECEPTOR-LIKE PROTEIN KINASE, PUTATIVE SIMILAR TO RECEPTOR-LIKE SERINE/THREONINE KINASE GB:AAC50043 GI:2465923 FROM [ARABIDOPSIS THALIANA] | Kinase, Protein |
| 4419 | 584 | RECEPTOR PROTEIN KINASE, PUTATIVE CONTAINS PFAM PROFILES: PF00069: EUKARYOTIC PROTEIN KINASE DOMAIN, MULTIPLE PF00560: LEUCINE RICH REPEAT | Kinase, Protein |
| 4436 | 585 | 3'-5' EXONUCLEASE, PUTATIVE CONTAINS PFAM PROFILE: PF01612: 3'-5' EXONUCLEASE | Nuclease |
| 4464 | 586 | TRIACYLGLYCEROL ACYLHYDROLASE GI:230348 FROM [RHIZOMUCOR MIEHEI][HYPOTHETICAL PROTEIN CONTAINS SIMILARITY TO] | Hydrolase |
| 4469 | 587 | CHITINASE, PUTATIVE SIMILAR TO CHITINASE GI:17798 FROM [BRASSICA NAPUS] | Chitinase |
| 4472 | 588 | POLYGALACTURONASE, PUTATIVE SIMILAR TO POLYGALACTURONASE PG1 GI:5669846 FROM [GLYCINE MAX] | Glycosylase |
| 4473 | 589 | RECEPTOR-LIKE PROTEIN KINASE GI:7529754 FROM [ARABIDOPSIS THALIANA], SIMILAR TO | Kinase, Protein |

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| 4480 | 590 | PECTINACETYLESTERASE PRECURSOR, PUTATIVE SIMILAR TO PECTINACETYLESTERASE PRECURSOR GI:1431629 FROM [VIGNA RADIATA] | Esterase |
| 4512 | 591 | ATP PHOSPHORIBOSYL TRANSFERASE IDENTICAL TO ATP PHOSPHORIBOSYL TRANSFERASE GI:6683617 FROM [ARABIDOPSIS THALIANA] | Transferases |
| 4518 | 592 | PHOSPHOGLYCERATE KINASE, PUTATIVE SIMILAR TO PHOSPHOGLYCERATE KINASE GI:155584 FROM [ZYMOMONAS MOBILIS] | Kinase |
| 4520 | 593 | CARBONIC ANHYDRASE, PUTATIVE SIMILAR TO CARBONIC ANHYDRASE 1 GI:882241 FROM [FLAVERIA LINEARIS] | Anhydrase |
| 4532 | 594 | GLUTAMYL-TRNA REDUCTASE, PUTATIVE SIMILAR TO GLUTAMYL-TRNA REDUCTASE GI:1694925 FROM [CUCUMIS SATIVUS] | Reductase |
| 4533 | 595 | HEME OXYGENASE PLASTID, PUTATIVE SIMILAR TO PLASTID HEME OXYGENASE GI:4877397 FROM [ARABIDOPSIS THALIANA] | Oxygenases |
| 4539 | 596 | AMINO ACID PERMEASE I IDENTICAL TO AMINO ACID PERMEASE I GI:22641 FROM [ARABIDOPSIS THALIANA] | Transporter |
| 4541 | 597 | XYLAN ENDOHYDROLASE, PUTATIVE SIMILAR TO (1,4)-BETA-XYLAN ENDOHYDROLASE GI:5306060 FROM [TRITICUM AESTIVUM] | Hydrolase |
| 4545 | 598 | PEPTIDYL-PROLYL ISOMERASE, PUTATIVE SIMILAR TO PEPTIDYLPROLYL ISOMERASE GI:9294180 FROM [ARABIDOPSIS THALIANA] | Isomerase |
| 4553 | 599 | XYLAN ENDOHYDROLASE ISOENZYME, PUTATIVE SIMILAR TO XYLAN ENDOHYDROLASE ISOENZYME X- I GI:1813594 FROM [HORDEUM VULGARE] | Hydrolase |
| 4571 | 600 | GLUTATHIONE S-TRANSFERASE, PUTATIVE SIMILAR TO GLUTATHIONE S-TRANSFERASE GB:AAF29773 GI:6856103 FROM [GOSSYPIMUM HIRSUTUM] | Transferases |
| 4573 | 601 | GLUTATHIONE S-TRANSFERASE, PUTATIVE SIMILAR TO GLUTATHIONE S-TRANSFERASE GI:2190991 FROM [AEGILOPS TAUSCHII] | Transferases |

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| 4578 | 602 | OLIGOPEPTIDE TRANSPORTER, PUTATIVE SIMILAR TO OLIGOPEPTIDE TRANSPORTER GI:510238 FROM [ARABIDOPSIS THALIANA] | Transporter |
| 4617 | 603 | POTASSIUM TRANSPORTER, PUTATIVE SIMILAR TO POTASSIUM TRANSPORTER GI:2654088 FROM [ARABIDOPSIS THALIANA] | Transporter |
| 4637 | 604 | POLYGALACTURONASE ISOENZYME 1 BETA SUBUNIT, PUTATIVE SIMILAR TO POLYGALACTURONASE ISOENZYME 1 BETA SUBUNIT GI:1762585 FROM [LYCOPERSICON ESCULENTUM] | Glycosylase |
| 4643 | 605 | GALACTINOL SYNTHASE, PUTATIVE SIMILAR TO GALACTINOL SYNTHASE GI:5608497 FROM [AJUGA REPTANS] | Synthase |
| 4645 | 606 | GALACTINOL SYNTHASE, PUTATIVE SIMILAR TO GALACTINOL SYNTHASE GI:5608497 FROM [AJUGA REPTANS] | Synthase |
| 4650 | 607 | 2-KETOCYCLOHEXANECARBOXYL-COA HYDROLASE GI:3243084 FROM [RHODOPSEUDOMONAS PALUSTRIS][HYPOTHETICAL PROTEIN CONTAINS SIMILARITY TO] | Hydrolase |
| 4653 | 608 | POLYGALACTURONASE, PUTATIVE SIMILAR TO POLYGALACTURONASE GI:9293940 FROM [ARABIDOPSIS THALIANA] | Glycosylase |
| 4655 | 609 | S-RIBONUCLEASE BINDING PROTEIN SBP1 GI:6760451 FROM [PETUNIA HYBRIDA] | Nuclease |
| 4657 | 610 | RECEPTOR KINASE, PUTATIVE SIMILAR TO RECEPTOR KINASE GI:498278 FROM [PETUNIA INTEGRIFOLIA] | Kinase, Protein |
| 4661 | 611 | D-ALA,D-ALA LIGASE GI:6634594 FROM [STREPTOCOCCUS PNEUMONIAE][HYPOTHETICAL PROTEIN CONTAINS SIMILARITY TO] | Ligase |
| 4674 | 612 | RECEPTOR-LIKE KINASE, PUTATIVE SIMILAR TO SOMATIC EMBRYOGENESIS RECEPTOR-LIKE KINASE GI:2224910 FROM [DAUCUS CAROTA] | Kinase, Protein |
| 4687 | 613 | IRON-REGULATED TRANSPORTER SIMILAR TO IRON-REGULATED TRANSPORTER 1 GB:AAD30548 FROM [LYCOPERSICON ESCULENTUM][PUTATIVE] | Transporter |

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| 4689 | 614 | GIBBERELLIN 20-OXIDASE SIMILAR TO GIBBERELLIN 20-OXIDASE GB:CAA58295 FROM [ARABIDOPSIS THALIANA][PUTATIVE] | Oxidase |
| 4690 | 615 | AMINOMETHYLTRANSFERASE GB:CAA20175 FROM [STREPTOMYCES COELICOLOR A3(2)]; HYPOTHETICAL PROTEIN PREDICTED BY GENSCAN+, SIMILAR TO | Transferases |
| 4702 | 616 | S-LINALOOL SYNTHASE, PUTATIVE SIMILAR TO S-LINALOOL SYNTHASE GI:1491939 FROM [CLARKIA BREWERI] | Synthase |
| 4715 | 617 | SECRETORY CARRIER MEMBRANE PROTEIN IDENTICAL TO SECRETORY CARRIER MEMBRANE PROTEIN GI:7109228 FROM [ARABIDOPSIS THALIANA] | Transporter |
| 4717 | 618 | LYSINE AND HISTIDINE SPECIFIC TRANSPORTER, PUTATIVE SIMILAR TO LYSINE AND HISTIDINE SPECIFIC TRANSPORTER GI:2576361 FROM [ARABIDOPSIS THALIANA] | Transporter |
| 4726 | 619 | RECEPTOR PROTEIN KINASE (IRK1), PUTATIVE SIMILAR TO RECEPTOR PROTEIN KINASE (IRK1) GI:836953 FROM [IPOMOEA TRIFIDA] | Kinase, Protein |
| 4727 | 620 | RECEPTOR PROTEIN KINASE (IRK1), PUTATIVE SIMILAR TO RECEPTOR PROTEIN KINASE (IRK1) GI:836953 FROM [IPOMOEA TRIFIDA] | Kinase, Protein |
| 4728 | 621 | SERINE/THREONINE KINASE GI:4585880 FROM [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN SIMILAR TO][PUTATIVE] | Kinase, Protein |
| 4729 | 622 | RECEPTOR KINASE, PUTATIVE SIMILAR TO RECEPTOR KINASE GI:166692 FROM [ARABIDOPSIS THALIANA] | Kinase, Protein |
| 4730 | 623 | RECEPTOR KINASE, PUTATIVE SIMILAR TO RECEPTOR KINASE I GI:2662048 FROM [BRASSICA RAPA] | Kinase, Protein |
| 4732 | 624 | RECEPTOR KINASE, PUTATIVE SIMILAR TO RECEPTOR KINASE GI:166692 FROM [ARABIDOPSIS THALIANA] | Kinase, Protein |
| 4733 | 625 | RECEPTOR KINASE, PUTATIVE SIMILAR TO RECEPTOR KINASE GI:166692 FROM [ARABIDOPSIS THALIANA] | Kinase, Protein |
| 4734 | 626 | RECEPTOR KINASE, PUTATIVE SIMILAR TO RECEPTOR KINASE GI:166692 FROM [ARABIDOPSIS THALIANA] | Kinase, Protein |

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| 4736 | 627 | RECEPTOR KINASE, PUTATIVE SIMILAR TO RECEPTOR KINASE GI:166692 FROM [ARABIDOPSIS THALIANA] | Kinase, Protein |
| 4738 | 628 | RECEPTOR PROTEIN KINASE (IRK1), PUTATIVE SIMILAR TO RECEPTOR PROTEIN KINASE (IRK1) GI:836953 FROM [POMOEIA TRIFIDA] | Kinase, Protein |
| 4739 | 629 | RECEPTOR KINASE, PUTATIVE SIMILAR TO RECEPTOR KINASE GI:166692 FROM [ARABIDOPSIS THALIANA] | Kinase, Protein |
| 4740 | 630 | RECEPTOR KINASE, PUTATIVE SIMILAR TO RECEPTOR KINASE GI:166692 FROM [ARABIDOPSIS THALIANA] | Kinase, Protein |
| 4744 | 631 | RECEPTOR KINASE, PUTATIVE SIMILAR TO RECEPTOR KINASE GI:166692 FROM [ARABIDOPSIS THALIANA] | Kinase, Protein |
| 4748 | 632 | SERINE/THREONINE PROTEIN KINASE, PUTATIVE SIMILAR TO SERINE/THREONINE PROTEIN KINASE GI:1066501 FROM [ARABIDOPSIS THALIANA] | Kinase, Protein |
| 4750 | 633 | RECEPTOR-LIKE KINASE, PUTATIVE SIMILAR TO RECEPTOR-LIKE KINASE GI:1783311 FROM [BRASSICA OLERACEA] | Kinase, Protein |
| 4752 | 634 | INOSINE-GUANOSINE NUCLEOSIDE TRANSPORTER GI:8272582 FROM [LEISHMANIA DONOVANI][HYPOTHETICAL PROTEIN CONTAINS SIMILARITY TO] | Transporter |
| 4756 | 635 | CINEOLE SYNTHASE, PUTATIVE SIMILAR TO 1,8-CINEOLE SYNTHASE GI:3309117 FROM [SALVIA OFFICINALIS] | Synthase |
| 4760 | 636 | DIHYDROFLAVONOL 4-REDUCTASE, PUTATIVE SIMILAR TO DIHYDROFLAVONOL 4-REDUCTASE GI:1332411 FROM [ROSA HYBRIDA] | Reductase |
| 4763 | 637 | SERINE/THREONINE PROTEIN KINASE, PUTATIVE SIMILAR TO SERINE/THREONINE PROTEIN KINASE GI:3080385 FROM [ARABIDOPSIS THALIANA] | Kinase, Protein |
| 4774 | 638 | PROTEIN KINASE, PUTATIVE SIMILAR TO PROTEIN KINASE GI:9294282 FROM [ARABIDOPSIS THALIANA] | Kinase, Protein |
| 4795 | 639 | RECEPTOR-LIKE PROTEIN KINASE GI:3461841 FROM [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN SIMILAR TO][PUTATIVE] | Kinase, Protein |

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| 4796 | 640 | RECEPTOR-LIKE PROTEIN KINASE, PUTATIVE SIMILAR TO RECEPTOR-LIKE PROTEIN KINASE GI:9758833 FROM [ARABIDOPSIS THALIANA] | Kinase, Protein |
| 4804 | 641 | 5'-ADENYLYLPHOSPHOSULFATE REDUCTASE, PUTATIVE SIMILAR TO 5'-ADENYLYLPHOSPHOSULFATE REDUCTASE GI:1336168 FROM [ARABIDOPSIS THALIANA] | Reductase |
| 4810 | 642 | PEROXIDASE ISOZYME GI:217933 FROM [ARMORACIA RUSTICANA] UNKNOWN PROTEIN CONTAINS SIMILARITY TO | Oxidase |
| 4823 | 643 | ACC OXIDASE, PUTATIVE SIMILAR TO ACC OXIDASE GI:587086 FROM [BRASSICA OLERACEA] | Oxidase |
| 4843 | 644 | GLUCOSE 1-DEHYDROGENASE (AB000617); SIMILAR TO EST GB T88100 SIMILAR TO OXIDOREDUCTASE-LIKE PROTEIN GB:CAB75763 GI:7019662 FROM [ARABIDOPSIS THALIANA][SIMILAR TO] | Dehydrogenases |
| 4846 | 645 | 3-KETOACYL-ACYL CARRIER PROTEIN SYNTHASE III (KAS III) IDENTICAL TO 3-KETOACYL-ACYL CARRIER PROTEIN SYNTHASE III (KAS III) GB:CAA72385 GI:1888359 [ARABIDOPSIS THALIANA] | Synthase |
| 4863 | 646 | AMINE OXIDASE, PUTATIVE SIMILAR TO AMINE OXIDASE GB:AAD49420 GI:5733089 [CANAVALLIA LINEATA] | Oxidase |
| 4871 | 647 | NON-LTR REVERSE TRANSCRIPTASE, PUTATIVE SIMILAR TO MANY PREDICTED NON-LTR REVERSE TRANSCRIPTASES | Transcriptase |
| 4872 | 648 | O-METHYLTRANSFERASE 1, PUTATIVE SIMILAR TO GB:AAB96879 FROM [ARABIDOPSIS THALIANA] (BIOCHIM. BIOPHYS. ACTA 1353 (3), 199-202 (1997)) | Transferases |
| 4877 | 649 | PROTEIN KINASE, PUTATIVE CONTAINS PROTEIN KINASE DOMAINS | Kinase, Protein |
| 4878 | 650 | 1-AMINOCYCLOPROPANE-1-CARBOXYLATE SYNTHASE, PUTATIVE SIMILAR TO GB:U35779 FROM [TRITICUM AESTIVUM] (PLANT MOL. BIOL. 31 (5), 1009-1020 (1996)) | Synthase |

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| 4896 | 651 | CAFFEIC O-METHYLTRANSFERASE, PUTATIVE SIMILAR TO GI:602587 FROM [PRUNUS DULCIS] (PLANT PHYSIOL. 108, 1341-1341 (1995)) | Transferases |
| 4921 | 652 | GLUCOSE 1-DEHYDROGENASE GB:P40288 FROM [BACILLUS MEGATERIUM], REDUCTASE, PUTATIVE SIMILAR TO | Dehydrogenases |
| 4926 | 653 | RECEPTOR PROTEIN KINASE, PUTATIVE CONTAINS PFAM PROFILES: PF00069 EUKARYOTIC PROTEIN KINASE DOMAIN, PF00560 LEUCINE RICH REPEAT | Kinase, Protein |
| 4933 | 654 | PROTEIN KINASE, PUTATIVE CONTAINS PFAM PROFILE: PF00069 EUKARYOTIC PROTEIN KINASE DOMAIN | Kinase, Protein |
| 4948 | 655 | UDP-N-ACETYLMURAMOYLALANYL-D-GLUTAMATE- 2,6-DIAMINOPIMELATE LIGASE SIMILAR TO UDP-N- ACETYLMURAMOYLALANYL-D-GLUTAMATE-2,6- DIAMINOPIMELATE LIGASE (MURE) GB:S40595 [ESCHERICHIA COLI][PUTATIVE] | Ligase |
| 4956 | 656 | AMINOPEPTIDASE SIMILAR TO AMINOPEPTIDASE N (ALPHA-AMINOACYLPEPTIDE HYDROLASE) GB:P04825 [ESCHERICHIA COLI]; CONTAINS PFAM PROFILE: PF00099 ZINC-BINDING METALLOPROTEASE DOMAIN[PUTATIVE] | Protease |
| 4970 | 657 | MONODEHYDROASCORBATE REDUCTASE SIMILAR TO MONODEHYDROASCORBATE REDUCTASE GB:AAD28178 [BRASSICA JUNCEA][PUTATIVE] | Reductase |
| 5024 | 658 | PEPTIDE TRANSPORTER, PUTATIVE PREDICTED BY GENEMARK.HMM | Transporter |
| 5049 | 659 | BETA-1,3-GLUCANASE, PUTATIVE SIMILAR TO BETA- 1,3-GLUCANASE GI:8843743 FROM [ARABIDOPSIS THALIANA] | Glycosylase |
| 5059 | 660 | RNA POLYMERASE SIGMA-SUBUNIT IDENTICAL TO PLASTID RNA POLYMERASE SIGMA-SUBUNIT GI:2398851 FROM [ARABIDOPSIS THALIANA] | Polymerase |
| 5064 | 661 | RHAMNOSYLTRANSFERASE, PUTATIVE SIMILAR TO RHAMNOSYLTRANSFERASE GI:454252 FROM [PETUNIA HYBRIDA] | Transferases |

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| 5065 | 662 | ANTHOCYANIDIN-3-GLUCOSIDE RHAMNOSYLTRANSFERASE, PUTATIVE SIMILAR TO ANTHOCYANIDIN-3-GLUCOSIDE RHAMNOSYLTRANSFERASE GI:397567 FROM [PETUNIA HYBRIDA] | Transferases |
| 5070 | 663 | GAMMA-TOCOPHEROL METHYLTRANSFERASE ALMOST IDENTICAL TO GAMMA-TOCOPHEROL METHYLTRANSFERASE GI:4106538 FROM [ARABIDOPSIS THALIANA] | Transferases |
| 5091 | 664 | SERINE THREONINE KINASE GI:166813 FROM [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN CONTAINS SIMILARITY TO] | Kinase, Protein |
| 5096 | 665 | ASPARTYL PROTEASE GI:6728988 FROM [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN SIMILAR TO][PUTATIVE] | Protease |
| 5097 | 666 | SERINE THREONINE KINASE GI:166813 FROM [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN CONTAINS SIMILARITY TO] | Kinase, Protein |
| 5103 | 667 | XYLOGLUCAN ENDOTRANSGLYCOSYLASE, PUTATIVE SIMILAR TO XYLOGLUCAN ENDOTRANSGLYCOSYLASE 1 GI:3901012 FROM [FAGUS SYLVATICA] | Glycosylase |
| 5114 | 668 | ANTIGEN RECEPTOR, PUTATIVE SIMILAR TO ANTIGEN RECEPTOR GI:3982955 FROM [GINGLYMOSTOMA CIRRATUM] | Receptor |
| 5123 | 669 | CARNITINE RACEMASE LIKE PROTEIN GI:7268149 FROM [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN SIMILAR TO] | Epimerase |
| 5128 | 670 | POLYGALACTURONASE, PUTATIVE SIMILAR TO POLYGALACTURONASE GI:2605891 FROM [LYCOPERSICON ESCULENTUM] | Glycosylase |
| 5129 | 671 | INOSITOL POLYPHOSPHATE 5'-PHOSPHATASE GI:3212848 FROM [ARABIDOPSIS THALIANA], SIMILAR TO PUTATIVE | Phosphatase |
| 5134 | 672 | SERINE PROTEASE DO, PUTATIVE SIMILAR TO PROTEASE DO (HTRA) SP:P09376 [ESCHERICHIA COLI] | Protease |

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| 5135 | 673 | SERINE PROTEASE DO, PUTATIVE SIMILAR TO PROTEASE DO (HTRA) SP:P09376 [ESCHERICHIA COLI] | Protease |
| 5150 | 674 | RECEPTOR KINASE, PUTATIVE SIMILAR TO RECEPTOR KINASE 1 [BRASSICA RAPA] GB:BAA23676 | Kinase, Protein |
| 5151 | 675 | RECEPTOR KINASE, PUTATIVE SIMILAR TO RECEPTOR KINASE 1 [BRASSICA RAPA] GB:BAA23676 | Kinase, Protein |
| 5166 | 676 | GLUTAMATE DECARBOXYLASE (GAD), PUTATIVE SIMILAR TO GLUTAMATE DECARBOXYLASE (GAD) GI:294111 FROM [PETUNIA HYBRIDA] | Decarboxylase |
| 5171 | 677 | TERPENE SYNTHASE, PUTATIVE CONTAINS PFAM PROFILE: PF01397: TERPENE SYNTHASE FAMILY | Synthase |
| 5182 | 678 | OXIDOREDUCTASE, PUTATIVE CONTAINS PFAM PROFILE: PF01408: OXIDOREDUCTASE, GFO/IDH/MOCA FAMILY | Reductase |
| 5184 | 679 | RECEPTOR PROTEIN KINASE (TMK1), PUTATIVE SIMILAR TO PUTATIVE RECEPTOR PROTEIN KINASE (TMK1) [ARABIDOPSIS THALIANA (MOUSE-EAR CRESS)] SP:P43298 | Kinase, Protein |
| 5194 | 680 | BETA-1,3-GLUCANASE PRECURSOR, PUTATIVE SIMILAR TO GI:4097948 FROM [ORYZA SATIVA] (GENE 223 (1-2), 311-320 (1998)) | Glycosylase |
| 5212 | 681 | FRUCTOKINASE, PUTATIVE SIMILAR TO FRUCTOKINASE [LYCOPERSICON ESCULENTUM] GI:2102691 | Kinase |
| 5215 | 682 | PROTEIN KINASE, PUTATIVE CONTAINS PFAM PROFILE: PF00069: EUKARYOTIC PROTEIN KINASE DOMAIN | Kinase, Protein |
| 5221 | 683 | FORMYL TRANSFERASE, PUTATIVE CONTAINS PFAM PROFILE: PF00551: FORMYL TRANSFERASE | Transferases |
| 5226 | 684 | SUCROSE-PROTON SYMPORTER, 5' PARTIAL SIMILAR TO C-TERM OF SUCROSE-PROTON SYMPORTER [ARABIDOPSIS THALIANA] GI:407094 | Transporter |
| 5248 | 685 | CINNAMYL ALCOHOL DEHYDROGENASE, PUTATIVE SIMILAR TO CINNAMYL ALCOHOL DEHYDROGENASE [EUCALYPTUS GUNNII] GI:1143445 | Dehydrogenases |

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| 5251 | 686 | RECEPTOR PROTEIN KINASE, PUTATIVE CONTAINS PFAM PROFILES: PF00069: EUKARYOTIC PROTEIN KINASE DOMAIN, MULTIPLE PF00560: LEUCINE RICH REPEAT | Kinase, Protein |
| 5256 | 687 | PROTEIN KINASE, PUTATIVE CONTAINS PFAM PROFILE: PF00069: EUKARYOTIC PROTEIN KINASE DOMAIN | Kinase, Protein |
| 5259 | 688 | RECEPTOR SERINE/THREONINE KINASE PR5K, PUTATIVE SIMILAR TO RECEPTOR SERINE/THREONINE KINASE PR5K GI:1235680 FROM [ARABIDOPSIS THALIANA] | Kinase, Protein |
| 5260 | 689 | RECEPTOR SERINE/THREONINE KINASE PR5K, PUTATIVE SIMILAR TO RECEPTOR SERINE/THREONINE KINASE PR5K GI:1235680 FROM [ARABIDOPSIS THALIANA] | Kinase, Protein |
| 5261 | 690 | RECEPTOR SERINE/THREONINE KINASE PR5K, PUTATIVE SIMILAR TO RECEPTOR SERINE/THREONINE KINASE PR5K GI:1235680 FROM [ARABIDOPSIS THALIANA] | Kinase, Protein |
| 5266 | 691 | KINASE, PUTATIVE SIMILAR TO LEAF RUST RESISTANCE KINASE LR10 GI:1680685 FROM [TRITICUM AESTIVUM] | Kinase, Protein |
| 5267 | 692 | RECEPTOR-LIKE KINASE, PUTATIVE SIMILAR TO RECEPTOR-LIKE KINASE GI:5523856 FROM [HORDEUM VULGARE] | Kinase, Protein |
| 5275 | 693 | RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL UNIT, PUTATIVE SIMILAR TO RIBULOSE-BISPHOSPHATE CARBOXYLASE SMALL UNIT GI:406726 FROM [BRASSICA NAPUS] | Carboxylase |
| 5292 | 694 | GLYOXAL OXIDASE (GLX1), PUTATIVE SIMILAR TO GLYOXAL OXIDASE (GLX1) GI:1050301 FROM [PHANEROCHAETE CHRYSOSPORIUM] | Oxidase |
| 5309 | 695 | PROTEIN KINASE PFAM HMM HIT: EUKARYOTIC PROTEIN KINASE DOMAIN; IDENTICAL TO GB:AAC18787 [ARABIDOPSIS THALIANA][PUTATIVE] | Kinase, Protein |

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| 5313 | 696 | RECEPTOR-LIKE PROTEIN KINASE GI:4262228 FROM [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN SIMILAR TO][PUTATIVE] | Kinase, Protein |
| 5314 | 697 | RECEPTOR KINASE, PUTATIVE SIMILAR TO RECEPTOR KINASE 1 GI:9294449 FROM [ARABIDOPSIS THALIANA] | Kinase, Protein |
| 5325 | 698 | AMINO ACID PERMEASE SIMILAR TO LYSINE AND HISTIDINE SPECIFIC TRANSPORTER GB:AAC49885 [ARABIDOPSIS THALIANA][PUTATIVE] | Transporter |
| 5330 | 699 | AMINO ACID PERMEASE, PUTATIVE SIMILAR TO AMINO ACID PERMEASE 1 GB: AAB48944 GI:976402 FROM [NICOTIANA SYLVESTRIS] | Transporter |
| 5341 | 700 | RECEPTOR PROTEIN KINASE, PUTATIVE SIMILAR TO LIGHT REPRESSIBLE RECEPTOR PROTEIN KINASE GB:CAA66376 GI:1321686 FROM [ARABIDOPSIS THALIANA] | Kinase, Protein |
| 5344 | 701 | ENDOCHITINASE, PUTATIVE SIMILAR TO PECTATE LYASE 1 GB:AAF19195 GI:6606532 FROM [MUSA ACUMINATA] | Chitinase |
| 5346 | 702 | ABC TRANSPORTER SIMILAR TO TERMINAL EAR1 GB:AAC39463 GI:3153237 FROM [ZEA MAYS] (NATURE 393 (6681), 166-168 (1998))[PUTATIVE] | Transporter |
| 5358 | 703 | N-ACETYLGLUCOSAMINYLTRANSFERASE III GB:AAC53064 [MUS MUSCULUS], UNKNOWN PROTEIN SIMILAR TO | Transferases |
| 5368 | 704 | S-ADENOSYL-L-METHIONINE:TRANS-CAFFEoyl-COENZYME A 3-O-METHYLTRANSFERASE SIMILAR TO S-ADENOSYL-L-METHIONINE:TRANS-CAFFEoyl-COENZYME A 3-O-METHYLTRANSFERASE GB:AAA62426 [ARABIDOPSIS THALIANA] (FUNCTION=DISEASE RESISTANCE)[PUTATIVE] | Transferases |
| 5369 | 705 | S-ADENOSYL-L-METHIONINE:TRANS-CAFFEoyl-COENZYME A 3-O-METHYLTRANSFERASE SIMILAR TO S-ADENOSYL-L-METHIONINE:TRANS-CAFFEoyl-COENZYME A 3-O-METHYLTRANSFERASE GB:AAA62426 [ARABIDOPSIS THALIANA] (FUNCTION=DISEASE RESISTANCE)[PUTATIVE] | Transferases |

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| 5370 | 706 | PHOSPHATIDYLINOSITOL SYNTHASE (PIS1) IDENTICAL TO PHOSPHATIDYLINOSITOL SYNTHASE (PIS1) GB:AJ000539 | Synthase |
| 5371 | 707 | HYDROXYPYRUVATE REDUCTASE (HPR) IDENTICAL TO HYDROXYPYRUVATE REDUCTASE (HPR) GB:D85339 [ARABIDOPSIS THALIANA] (PLANT CELL PHYSIOL 1997 APR;38(4):449-55) | Reductase |
| 5374 | 708 | S-ADENOSYL-L-METHIONINE:SALICYLIC ACID CARBOXYL METHYLTRANSFERASE SIMILAR TO S- ADENOSYL-L-METHIONINE:SALICYLIC ACID CARBOXYL METHYLTRANSFERASE GB:AAF00108 [CLARKIA BREWERI] (ENZYME INVOLVED IN FLORAL SCENT PRODUCTION AND PLANT DEFENSE)[PUTATIVE] | Transferases |
| 5399 | 709 | BIFUNCTIONAL NUCLEASE SIMILAR TO BIFUNCTIONAL NUCLEASE GB:AAD00694 FROM [ZINNIA ELEGANS][PUTATIVE] | Nuclease |
| 5410 | 710 | RECEPTOR KINASE SIMILAR TO RECEPTOR KINASE GB:AAA33715 FROM [PETUNIA INTEGRIFOLIA][PUTATIVE] | Kinase, Protein |
| 5411 | 711 | PROTEIN PHOSPHATASE SIMILAR TO PROTEIN PHOSPHATASE-2C GB:AAC36697 FROM [MESEMBRYANTHEMUM CRYSTALLINUM][PUTATIVE] | Phosphatase |
| 5412 | 712 | ASPARAGINYL-TRNA SYNTHETASE SIMILAR TO SYN1 PROTEIN GB:AAD46681[PUTATIVE] | Synthase |
| 5416 | 713 | TRNA ISOPENTENYL TRANSFERASE SIMILAR TO TRNA ISOPENTENYL TRANSFERASE GB:AAF00582 [ARABIDOPSIS THALIANA]; CONTAINS PFAM PROFILE: PF01715 IPP TRANSFERASE (TRNA DELTA(2)- ISOPENTENYLPYROPHOSPHATE TRANSFERASE)[PUTATIVE] | Transferases |
| 5424 | 714 | CINNAMOYL COA REDUCTASE GB:CAA12276 [POPULUS BALSAMIFERA SUBSP. TRICHOCARPA], ALDEHYDE REDUCTASE GB:AAD53967 [VIGNA RADIATA], DIHYDROFLAVONOL 4-REDUCTASE GB:BAA12723 [ROSA HYBRIDA][PUTATIVE] | Reductase |

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| 5439 | 715 | PROTEIN KINASE, PUTATIVE SIMILAR TO PROTEIN KINASE 1 GB:BAA94509 GI:7573596 FROM [POPULUS NIGRA] | Kinase, Protein |
| 5441 | 716 | ATPASE, PUTATIVE SIMILAR TO CHROMAFFIN GRANULE ATPASE II GB:AAD03352 GI:4115341 FROM [BOS TAURUS] | ATPase |
| 5442 | 717 | CYTIDINE AND DEOXYCYTIDYLATE DEAMINASE ZINC-BINDING REGION [UNKNOWN PROTEIN CONTAINS PFAM PROFILE: PF00383] | Deaminase |
| 5446 | 718 | PHOSPHOENOLPYRUVATE CARBOXYLASE SIMILAR TO PHOSPHOENOLPYRUVATE CARBOXYLASE GB:CAA11415 [BRASSICA JUNCEA]; CONTAINS PFAM PROFILE: PF00311 PHOSPHOENOLPYRUVATE CARBOXYLASE[PUTATIVE] | Carboxylase |
| 5453 | 719 | PROTEIN KINASE PFAM HMM HIT: EUKARYOTIC PROTEIN KINASE DOMAIN[PUTATIVE] | Kinase, Protein |
| 5455 | 720 | PEROXIDASE ATP23A IDENTICAL TO PEROXIDASE ATP23A GB:CAA70035 [ARABIDOPSIS THALIANA] | Oxidase |
| 5458 | 721 | 2-SUCCINYL-6-HYDROXY-2,4-CYCLOHEXADIENE-1-CARBOXYLIC ACID SYNTHASE / 2-OXOGLUTARATE DECARBOXYLASE, MENAQUINONE BIOSYNTHESIS PROTEIN SIMILAR TO MENAQUINONE BIOSYNTHESIS PROTEIN GB:P23970 [BACILLUS SUBTILIS]; PFAM HMM HIT: [PUTATIVE] | Synthase |
| 5482 | 722 | DIHYDROPTERIN PYROPHOSPHOKINASE, PUTATIVE SIMILAR TO DIHYDROPTERIN PYROPHOSPHOKINASE GI:1934971 FROM [PISUM SATIVUM] | Kinase |
| 5483 | 723 | FRUCTOKINASE SIMILAR TO FRUCTOKINASE GB:AAB57733 [LYCOPERSICON ESCULENTUM][PUTATIVE] | Kinase |
| 5487 | 724 | POLYNEURIDINE ALDEHYDE ESTERASE, PUTATIVE SIMILAR TO POLYNEURIDINE ALDEHYDE ESTERASE GI:6651393 FROM [RAUVOLFIA SERPENTINA] | Esterase |
| 5490 | 725 | RECEPTOR-LIKE PROTEIN KINASE SIMILAR TO PROTEIN KINASE GB:AAD11518 [ARABIDOPSIS THALIANA][PUTATIVE] | Kinase, Protein |

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| 5499 | 726 | CHORISMATE MUTASE, PUTATIVE CONTAINS PFAM PROFILE: PF01817: CHORISMATE MUTASE | Mutase |
| 5525 | 727 | STEROL DESATURASE CONTAINS PFAM PROFILE: PF01598 STEROL DESATURASE[PUTATIVE] | Desaturases |
| 5533 | 728 | HEME OXYGENASE SIMILAR TO HEME OXYGENASE GB:AAD22107 [ARABIDOPSIS THALIANA][PUTATIVE] | Oxygenases |
| 5534 | 729 | PROTEIN KINASE CONTAINS PFAM PROFILE: PF00069 EUKARYOTIC PROTEIN KINASE DOMAIN[PUTATIVE] | Kinase, Protein |
| 5544 | 730 | ALPHA-AMYLASE SIMILAR TO ALPHA-AMYLASE GB:AAA91884 [SOLANUM TUBEROSUM][PUTATIVE] | Glycosylase |
| 5546 | 731 | NITRATE TRANSPORTER (NTL1) IDENTICAL TO NITRATE TRANSPORTER (NTL1) GB:AAC28086 [ARABIDOPSIS THALIANA] | Transporter |
| 5547 | 732 | PEPTIDE TRANSPORTER SIMILAR TO PEPTIDE TRANSPORTER GB:AAC32034 [HORDEUM VULGARE][PUTATIVE] | Transporter |
| 5548 | 733 | PEPTIDE TRANSPORTER SIMILAR TO PEPTIDE TRANSPORTER GB:AAC32034 [HORDEUM VULGARE][PUTATIVE] | Transporter |
| 5552 | 734 | PROTEIN KINASE PFAM HMM HIT: EUKARYOTIC PROTEIN KINASE DOMAIN[PUTATIVE] | Kinase, Protein |
| 5553 | 735 | GLUTATHIONE TRANSFERASE SIMILAR TO GLUTATHIONE TRANSFERASE GB:CAA09188 [ALOPECURUS MYOSUROIDES][PUTATIVE] | Transferases |
| 5554 | 736 | GLUTATHIONE TRANSFERASE SIMILAR TO GLUTATHIONE TRANSFERASE GB:CAA09188 [ALOPECURUS MYOSUROIDES][PUTATIVE] | Transferases |
| 5555 | 737 | PECTIN METHYLESTERASE SIMILAR TO PECTIN METHYLESTERASE GB:CAA96435 [NICOTIANA PLUMBAGINIFOLIA][PUTATIVE] | Esterase |
| 5560 | 738 | RECEPTOR-LIKE PROTEIN KINASE, PUTATIVE SIMILAR TO RECEPTOR-LIKE PROTEIN KINASE GI:8777368 FROM [ARABIDOPSIS THALIANA] | Kinase, Protein |
| 5568 | 739 | VETISPIRADIENE SYNTHASE GI:9294376 FROM [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN SIMILAR TO] | Synthase |

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| 5569 | 740 | GLYCOSYL TRANSFERASE GI:7268597 FROM [ARABIDOPSIS THALIANA], UNKNOWN PROTEIN SIMILAR TO PUTATIVE | Transferases |
| 5571 | 741 | RECEPTOR-LIKE KINASE, PUTATIVE SIMILAR TO RECEPTOR-LIKE KINASE GI:1405837 FROM [ARABIDOPSIS THALIANA] | Kinase, Protein |
| 5573 | 742 | RECEPTOR-LIKE KINASE, PUTATIVE SIMILAR TO RECEPTOR-LIKE KINASE GI:1405837 FROM [ARABIDOPSIS THALIANA] | Kinase, Protein |
| 5585 | 743 | RECEPTOR SERINE/THREONINE KINASE PR5, PUTATIVE SIMILAR TO RECEPTOR SERINE/THREONINE KINASE PR5 GI:1235680 FROM [ARABIDOPSIS THALIANA] | Kinase, Protein |
| 5590 | 744 | POTASSIUM TRANSPORTER, PUTATIVE SIMILAR TO POTASSIUM TRANSPORTER GI:2654088 FROM [ARABIDOPSIS THALIANA] | Transporter |
| 5601 | 745 | CARBONIC ANHYDRASE, PUTATIVE SIMILAR TO CARBONIC ANHYDRASE GI:882241 FROM [FLAVERIA LINEARIS] | Anhydrase |
| 5605 | 746 | PROTEIN KINASE SIMILAR TO PROTEIN KINASE (APK1A) GB:Q06548 [ARABIDOPSIS THALIANA], IDENTICAL TO RESIDUES 1-319 OF SERINE/THREONINE KINASE-LIKE PROTEIN GB:AAC18796 [ARABIDOPSIS THALIANA]; PFAM HMM HIT: EUKARYOTIC PROTEIN KINASE DOMAIN[PUTATIVE] | Kinase, Protein |
| 5606 | 747 | PROTEIN KINASE SIMILAR TO C-TERMINAL REGION HAS SIMILARITY TO C-TERMINAL REGION OF PROTEIN KINASE (APK1A) GB:Q06548 [ARABIDOPSIS THALIANA]; PFAM HMM HIT: EUKARYOTIC PROTEIN KINASE DOMAIN[PUTATIVE] | Kinase, Protein |
| 5610 | 748 | POLYGALACTURONASE SIMILAR TO POLYGALACTURONASE PRECURSOR (PECTINASE) GB:P35336 [ACTINIDIA CHINENSIS][PUTATIVE] | Glycosylase |
| 5612 | 749 | PROTEIN KINASE SIMILAR TO C-TERMINAL REGION OF S-RECEPTOR KINASES GB:BAA21132, GB:BAA06285 [BRASSICA RAPA]; PFAM HMM HIT: EUKARYOTIC PROTEIN KINASE DOMAIN[PUTATIVE] | Kinase, Protein |

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| 5613 | 750 | PROTEIN KINASE SIMILAR TO C-TERMINAL REGION OF S-RECEPTOR KINASE PRECURSOR GB:JQ1677 [BRASSICA NAPUS]; PFAM HMM HIT: EUKARYOTIC PROTEIN KINASE DOMAIN[PUTATIVE] | Kinase, Protein |
| 5634 | 751 | PROTEIN KINASE CONTAINS PFAM PROFILE: PF00069 EUKARYOTIC PROTEIN KINASE DOMAIN[PUTATIVE] | Kinase, Protein |
| 5642 | 752 | PHOSPHOGLUCOMUTASE, PUTATIVE SIMILAR TO PHOSPHOGLUCOMUTASE GI:534981 FROM [SPINACIA OLERACEA] | Mutase |
| 5653 | 753 | AUXIN TRANSPORT PROTEIN REH1, PUTATIVE SIMILAR TO AUXIN TRANSPORT PROTEIN REH1 GI:3377509 FROM [ORYZA SATIVA] | Transporter |
| 5663 | 754 | BILIRUBIN OXIDASE SIMILAR TO; SPORE COAT PROTEIN-LIKE PROTEIN SIMILAR TO SPORE COAT PROTEIN A GB:P07788 FROM [BACILLUS SUBTILIS] AND GB:Q12737 [MYROTHECIUM VERRUCARIA] | Oxidase |
| 5666 | 755 | GLUCOSAMINYL (N-ACETYL) TRANSFERASE GB:4758422 FROM [HOMO SAPIENS], UNKNOWN PROTEIN SIMILAR TO | Transferases |
| 5675 | 756 | FATTY ACID ELONGASE 3-KETOACYL-COA SYNTHASE 1, KETOACYL-COA SYNTHASE SIMILAR TO, GB:AAC99312[PUTATIVE] | Synthase |
| 5676 | 757 | DEHYDROGENASE SIMILAR TO D-THREONINE DEHYDROGENASE GB:BAA34184[PUTATIVE] | Dehydrogenases |
| 5677 | 758 | DEHYDROGENASE SIMILAR TO D-THREONINE DEHYDROGENASE GB:BAA34184[PUTATIVE] | Dehydrogenases |
| 5681 | 759 | UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE SIMILAR TO UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR GB:Q09332 [DROSOPHILA MELANOGASTER][PUTATIVE] | Transferases |
| 5684 | 760 | LIPASE/HYDROLASE GDSL-LIKE MOTIF; PUTATIVE CONTAINS PFAM PROFILE: PF00657 LIPASE/ACYLHYDROLASE | Lipase |
| 5712 | 761 | AMINO ACID PERMEASE SIMILAR TO AMINO ACID PERMEASE GB:AAB48944 FROM [NICOTIANA SYLVESTRIS][PUTATIVE] | Transporter |

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| 5714 | 762 | LIPASE/HYDROLASE GDSL-motif SIMILAR TO PUTATIVE LIPASE/HYDROLASE GDSL- motifGB:AAC23769 AND GB:AAD12024[PUTATIVE] | Lipase |
| 5716 | 763 | PEROXIDASE ATP4A IDENTICAL TO GB:CAA67309 GI:1429213 FROM [ARABIDOPSIS THALIANA] | Oxidase |
| 5723 | 764 | HYPOXANTHINE RIBOSYL TRANSFERASE, PUTATIVE SIMILAR TO HYPOXANTHINE RIBOSYL TRANSFERASE GB:AAC46403 GI:2689037 FROM [VIBRIO PARAHAEMOLYTICUS] | Transferases |
| 5731 | 765 | PROTEIN KINASE, PUTATIVE SIMILAR TO RECEPTOR PROTEIN KINASE GB:BAA11869 GI:1389566 FROM [ARABIDOPSIS THALIANA] | Kinase, Protein |
| 5736 | 766 | SUCROSE TRANSPORT PROTEIN SUC1 IDENTICAL TO GB:S38197 FROM [ARABIDOPSIS THALIANA] | Transporter |
| 5737 | 767 | SUCROSE TRANSPORT PROTEIN SIMILAR TO SUCROSE TRANSPORT PROTEIN SUC1 GB:S38197 FROM [ARABIDOPSIS THALIANA][PUTATIVE] | Transporter |
| 5740 | 768 | HISTIDINOL-PHOSPHATE AMINOTRANSFERASE SIMILAR TO HISTIDINOL-PHOSPHATE AMINOTRANSFERASE GB:CAA70403 FROM [NICOTIANA TABACUM][PUTATIVE] | Transferases |
| 5747 | 769 | FUCOSYLTRANSFERASE 9 GB:NP_034373 FROM [MUS MUSCULUS], HYPOTHETICAL PROTEIN PREDICTED BY GENEFINDER, CONTAINS SIMILARITY TO | Transferases |
| 5761 | 770 | OLIGOPEPTIDE TRANSPORTER, PUTATIVE SIMILAR TO LEOPT1 [LYCOPERSICON ESCULENTUM] GI:4102839 | Transporter |
| 5766 | 771 | LEUCINE-RICH RECEPTOR-LIKE PROTEIN KINASE, PUTATIVE SIMILAR TO GI:3641252 FROM [MALUS X DOMESTICA] (PLANT MOL. BIOL. 40 (6), 945-957 (1999)) | Kinase, Protein |
| 5767 | 772 | PHOSPHOGLYCERATE DEHYDROGENASE, PUTATIVE CONTAINED WITHIN GI:6626247 FROM [ARCHAEOGLOBUS FULGIDUS] | Dehydrogenase |
| 5777 | 773 | LEUCINE-RICH RECEPTOR-LIKE PROTEIN KINASE, PUTATIVE SIMILAR TO GI:3641252 FROM [MALUS X DOMESTICA] (PLANT MOL. BIOL. 40 (6), 945-957 (1999)) | Kinase, Protein |

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| 5793 | 774 | RECEPTOR-LIKE PROTEIN KINASE CONTAINS PFAM PROFILES: PF00560 LEUCINE RICH REPEAT (5 COPIES), PF00069 EUKARYOTIC PROTEIN KINASE DOMAIN[PUTATIVE] | Kinase, Protein |
| 5801 | 775 | PROTEIN KINASE SIMILAR TO PROTEIN KINASE APK1A GB:Q06548 [ARABIDOPSIS THALIANA][PUTATIVE] | Kinase, Protein |
| 5815 | 776 | CINNAMYL-ALCOHOL DEHYDROGENASE SIMILAR TO CINNAMYL-ALCOHOL DEHYDROGENASE GB:AAC35846 [MEDICAGO SATIVA][PUTATIVE] | Dehydrogenases |
| 5817 | 777 | P-TYPE TRANSPORTING ATPASE SIMILAR TO ATPASE II GB:AAD34706 [HOMO SAPIENS][PUTATIVE] | Transporter |
| 5827 | 778 | THREONINE SYNTHASE, PUTATIVE SIMILAR TO THREONINE SYNTHASE GI:4850369 FROM [ARABIDOPSIS THALIANA] | Synthase |
| 5843 | 779 | MANDELONITRILE LYASE GI:288115 FROM [PRUNUS SEROTINA], UNKNOWN PROTEIN CONTAINS SIMILARITY TO | Lyase |
| 5851 | 780 | MANDELONITRILE LYASE, PUTATIVE SIMILAR TO MANDELONITRILE LYASE GI:288115 FROM [PRUNUS SEROTINA] | Lyase |
| 5862 | 781 | GLYCOSYL TRANSFERASE CONTAINS PFAM PROFILE: PF00534 GLYCOSYL TRANSFERASES GROUP I[PUTATIVE] | Transferases |
| 5880 | 782 | STEROID 22-ALPHA-HYDROXYLASE, PUTATIVE SIMILAR TO STEROID 22-ALPHA-HYDROXYLASE GI:2935342 FROM [ARABIDOPSIS THALIANA] | Hydroxylase |
| 5881 | 783 | GLUCOSIDASE II BETA-SUBUNIT GI:5452942 FROM [MUS MUSCULUS][HYPOTHETICAL PROTEIN CONTAINS SIMILARITY TO] | Glycosylase |
| 5883 | 784 | SUCROSE SYNTHASE, PUTATIVE SIMILAR TO SUCROSE SYNTHASE GI:4468151 FROM [CRATEROSTIGMA PLANTAGINEUM] | Synthase |
| 5893 | 785 | LYSOPHOSPHOLIPASE HOMOLOG, PUTATIVE SIMILAR TO LYSOPHOSPHOLIPASE HOMOLOG GI:2801536 FROM [ORYZA SATIVA] | Lipase |

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| 5898 | 786 | DIPHOSPHOINOSITOL POLYPHOSPHATE PHOSPHOHYDROLASE GI:3978224 FROM [HOMO SAPIENS], UNKNOWN PROTEIN CONTAINS SIMILARITY TO | Hydrolase |
| 5903 | 787 | AUXIN TRANSPORTER SPLICE VARIANT B, PUTATIVE SIMILAR TO GI:7109715 FROM [ARABIDOPSIS THALIANA] | Transporter |
| 5905 | 788 | LIPASE/HYDROLASE GDSL-LIKE MOTIF; PUTATIVE CONTAINS PFAM PROFILE: PF00657 LIPASE/ACYLHYDROLASE | Lipase |
| 5918 | 789 | UDP-N-ACETYLGLUCOSAMINE--N-ACETYLMURAMYL-(PENTAPEPTIDE)-PYROPHOSPHORYL-UNDECAPRENOL N-ACETYLGLUCOSAMINE TRANSFERASE SIMILAR TO PUTATIVE UDP-N-ACETYLGLUCOSAMINE--N-ACETYLMURAMYL-(PENTAPEPTIDE)-PYROPHOSPHORYL-UNDECAPRENOL N-ACETYLGLUCOSAMINE TRANSFERASE GB:007670 [ENTEROCOCCUS HIRAE][PUTATIVE] | Transferases |
| 5919 | 790 | ALPHA/BETA HYDROLASE FOLD | Hydrolase |
| 5932 | 791 | GLUCOSYLTRANSFERASE SIMILAR TO GLUCOSYLTRANSFERASE GB:AAB36653 FROM [NICOTIANA TABACUM][PUTATIVE] | Transferases |
| 5935 | 792 | LIPASE SIMILAR TO LIPASE GB:CAA74737 FROM [DROSOPHILA MELANOGASTER][PUTATIVE] | Lipase |
| 5941 | 793 | URIDINE KINASE GB:AAF09747 FROM [DEINOCOCCUS RADIODURANS], UNKNOWN PROTEIN CONTAINS A REGION SIMILAR TO | Kinase |
| 5942 | 794 | PROTEASE IV SIMILAR TO PROTEASE IV GB:AAA57008 FROM [ESCHERICHIA COLI][PUTATIVE] | Protease |
| 5943 | 795 | STRICTOSIDINE SYNTHASE SIMILAR TO STRICTOSIDINE SYNTHASE 3 PRECURSOR GB:P92976[PUTATIVE] | Synthase |
| 5944 | 796 | STRICTOSIDINE SYNTHASE SIMILAR TO STRICTOSIDINE SYNTHASE 1/2 PRECURSOR GB:P94111[PUTATIVE] | Synthase |

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| 5945 | 797 | STRICTOSIDINE SYNTHASE EXTREMELY SIMILAR TO STRICTOSIDINE SYNTHASE 1/2 PRECURSOR GB:P94111[PUTATIVE] | Synthase |
| 5947 | 798 | 2-ISOPROPYLMALATE SYNTHASE SIMILAR TO 2-ISOPROPYLMALATE SYNTHASE GB: AAB61598 FROM [LYCOPERSICON PENNELLII][PUTATIVE] | Synthase |
| 5950 | 799 | ADENOSINE KINASE (EC 2.7.1.20) GB:S52758 FROM [LEISHMANIA DONOVANI], HYPOTHETICAL PROTEIN PREDICTED BY GENSCAN+, SIMILAR TO | Kinase |
| 5952 | 800 | FLAVONOL SULFOTRANSFERASE SIMILAR TO FLAVONOL 4'-SULFOTRANSFERASE GB:P52837 FROM [FLAVERIA CHLORAEFOLIA][PUTATIVE] | Transferases |
| 5964 | 801 | GLYCEROPHOSPHODIESTER PHOSPHODIESTERASE SIMILAR TO GLYCEROPHOSPHORYL DIESTER PHOSPHODIESTERASE GB:AAF12F49 FROM [DEINOCOCCUS RADIODURANS][PUTATIVE] | Esterase |
| 5967 | 802 | MITOCHONDRIAL CARRIER PROTEIN SIMILAR TO GB:CAA21437 FROM [SCHIZOSACCHAROMYCES POMBE][PUTATIVE] | Transporter |
| 5979 | 803 | RECEPTOR PROTEIN KINASE SIMILAR TO BRASSINOSTEROID INSENSITIVE 1 GB:AAC49810 (PUTATIVE RECEPTOR PROTEIN KINASE); CONTAINS PFAM PROFILES: PF00560 LEUCINE RICH REPEAT (17 REPEATS), PF00069 EUKARYOTIC PROTEIN KINASE DOMAIN[PUTATIVE] | Kinase, Protein |
| 5981 | 804 | ALPHA GALACTOSYLTRANSFERASE SIMILAR TO ALPHA GALACTOSYLTRANSFERASE GB:CAB52246 [TRIGONELLA FOENUM-GRACUM] (PLANT CELL WALL MATRIX POLYSACCHARIDE BIOSYNTHESIS)[PUTATIVE] | Transferases |
| 5982 | 805 | EXONUCLEASE CONTAINS PFAM PROFILE: PF00929 EXONUCLEASE[PUTATIVE] | Nuclease |
| 5985 | 806 | XYLOGLUCAN FUCOSYLTRANSFERASE SIMILAR TO XYLOGLUCAN FUCOSYLTRANSFERASE GB:AAD41092 [ARABIDOPSIS THALIANA] (ENZYME INVOLVED IN PLANT CELL WALL BIOSYNTHESIS: SCIENCE 284, 1976-1979 (1999))[PUTATIVE] | Transferases |

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| 5989 | 807 | LIPASE/HYDROLASE GDSL-LIKE MOTIF; PUTATIVE CONTAINS PFAM PROFILE: PF00657 LIPASE/ACYLHYDROLASE | Lipase |
| 5990 | 808 | GERANYLGERANYL REDUCTASE IDENTICAL TO GERANYLGERANYL REDUCTASE GB:Y14044 [ARABIDOPSIS THALIANA] (INVOLVEMENT: CHLOROPHYLL, THE TOCOPHEROL AND THE PHYLLLOQUINONE PATHWAYS EUR J BIOCHEM 1998 JAN 15;251(1-2):413-7) | Reductase |
| 6001 | 809 | GLUTATHIONE S-TRANSFERASE SIMILAR TO PUTATIVE GLUTATHIONE S-TRANSFERASE GB:CAA10060 [ARABIDOPSIS THALIANA]; CONTAINS PFAM PROFILE: PF00043 GLUTATHIONE S- TRANSFERASES[PUTATIVE] | Transferases |
| 6005 | 810 | ALPHA/BETA HYDROLASE FOLD | Hydrolase |
| 6012 | 811 | ISOCHORISMATE SYNTHASE (ICSI) IDENTICAL TO ISOCHORISMATE SYNTHASE (ICSI) GB:AF078080 (CATALYZES CHORISMIC ACID TO ISOCHORISMIC ACID PLANT PHYSIOL. 118 (4), 1536 (1998)) | Synthase |
| 6013 | 812 | PHOSPHORIBOSYLANTHRANILATE TRANSFERASE, 3' PARTIAL SIMILAR TO PHOSPHORIBOSYLANTHRANILATE TRANSFERASE GB:CAA16616 [ARABIDOPSIS THALIANA][PUTATIVE] | Transferases |
| 6049 | 813 | DNA-3-METHYLADENINE GLYCOSYLASE I SIMILAR TO PUTATIVE DNA-3-METHYLADENINE GLYCOSYLASE I (TAG I) GB:P05100 [ESCHERICHIA COLI][PUTATIVE] | Glycosylase |
| 6063 | 814 | 3-METHYLADENINE DNA GLYCOSYLASE, PUTATIVE SIMILAR TO GI:1669515 FROM [SCHIZOSACCHAROMYCES POMBE] (GENE 177 (1-2), 229-235 (1996)) | Glycosylase |
| 6067 | 815 | GSH-DEPENDENT DEHYDROASCORBATE REDUCTASE 1, PUTATIVE SIMILAR TO GI:6939839 FROM [ORYZA SATIVA] | Reductase |
| 6068 | 816 | NADPH OXIDOREDUCTASE, PUTATIVE SIMILAR TO GI:1708420 FROM [ARABIDOPSIS THALIANA] (J. BIOL. CHEM. 270 (44), 26224-26231 (1995)) | Reductase |

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| 6069 | 817 | NADPH OXIDOREDUCTASE, PUTATIVE SIMILAR TO GI:1708420 FROM [ARABIDOPSIS THALIANA] (J. BIOL. CHEM. 270 (44), 26224-26231 (1995)) | Reductase |
| 6070 | 818 | NADPH OXIDOREDUCTASE, PUTATIVE SIMILAR TO GI:1708420 FROM [ARABIDOPSIS THALIANA] (J. BIOL. CHEM. 270 (44), 26224-26231 (1995)) | Reductase |
| 6084 | 819 | CYTOKININ OXIDASE, PUTATIVE SIMILAR TO GB:CAA77151 FROM [ZEA MAYS] (PLANT J. 17 (6), 615- 626 (1999)) | Oxidase |
| 6085 | 820 | PROTEASE, PUTATIVE SIMILAR TO SP:P36774 FROM [MYXOCOCCUS XANTHUS] | Protease |
| 6101 | 821 | RECEPTOR-LIKE PROTEIN KINASE, PUTATIVE RECEPTOR-LIKE PROTEIN KINASE GB:AAB36558 GI:1684913 FROM [IPOMOEA NIL] | Kinase, Protein |
| 6114 | 822 | PECTINESTERASE, PUTATIVE SIMILAR TO PECTINESTERASE GB:CAB08077 GI:1944575 FROM [LYCOPERSICON ESCULENTUM] | Esterase |
| 6117 | 823 | RECEPTOR KINASE (CLV1) IDENTICAL TO RECEPTOR KINASE (CLV1) GB:AAB58929 GI:2160756 [ARABIDOPSIS THALIANA] | Kinase, Protein |
| 6139 | 824 | RNA PSEUDOURIDYLATE SYNTHASE, PUTATIVE CONTAINS PFAM PROFILE: PF00849 RNA PSEUDOURIDYLATE SYNTHASE | Synthase |
| 6143 | 825 | S-ADENOSYL-METHIONINE-STEROL-C- METHYLTRANSFERASE, PUTATIVE ALMOST IDENTICAL TO S-ADENOSYL-METHIONINE-STEROL-C- METHYLTRANSFERASE GI:2246456 FROM [ARABIDOPSIS THALIANA] | Transferases |
| 6146 | 826 | PSEUDOURIDYLATE SYNTHASE 2 GI:1403092 FROM [SACCHAROMYCES CEREVISIAE][HYPOTHETICAL PROTEIN CONTAINS SIMILARITY TO] | Synthase |
| 6147 | 827 | ALPHA-AMYLASE, PUTATIVE SIMILAR TO ALPHA- AMYLASE GI:7532799 FROM [MALUS DOMESTICA] | Glycosylase |
| 6150 | 828 | PECTINESTERASE, PUTATIVE SIMILAR TO PECTINESTERASE GI:1944574 FROM [LYCOPERSICON ESCULENTUM] | Esterase |

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| 6170 | 829 | PROTEIN KINASE SIMILAR TO PROTEIN KINASE (APK1A); CONTAINS PFAM PROFILE: PF00069 EUKARYOTIC PROTEIN KINASE DOMAIN[PUTATIVE] | Kinase, Protein |
| 6176 | 830 | PHOSPHATE TRANSPORTER SIMILAR TO PHOSPHATE TRANSPORTER GB:BAA20522 [CATHARANTHUS ROSEUS][PUTATIVE] | Transporter |
| 6180 | 831 | CINNAMOYL-COA REDUCTASE SIMILAR TO CINNAMOYL-COA REDUCTASE GB:CAA56103 [EUCALYPTUS GUNNII][PUTATIVE] | Reductase |
| 6188 | 832 | PHOSPHOFRUCTO-1-KINASE, PYROPHOSPHATE-DEPENDENT PHOSPHOFRUCTOKINASE ALPHA SUBUNIT SIMILAR TO PYROPHOSPHATE-DEPENDENT PHOSPHOFRUCTOKINASE ALPHA SUBUNIT GB:AAD30596 [ARABIDOPSIS THALIANA][PUTATIVE] | Kinase |
| 6201 | 833 | 12-OXOPHYTODIENOATE REDUCTASE (OPR1) IDENTICAL TO 12-OXOPHYTODIENOATE REDUCTASE OPR1 GB:AAC78440 [ARABIDOPSIS THALIANA] | Reductase |
| 6202 | 834 | 12-OXOPHYTODIENOATE REDUCTASE (OPR2) IDENTICAL TO 12-OXOPHYTODIENOATE REDUCTASE OPR2 GB:AAC78441 [ARABIDOPSIS THALIANA] | Reductase |
| 6212 | 835 | CATECHOL O-METHYLTRANSFERASE SIMILAR TO CATECHOL O-METHYLTRANSFERASE GB:CAA55358 [VANILLA PLANIFOLIA][PUTATIVE] | Transferases |
| 6232 | 836 | URIDYLYL TRANSFERASE GI:4406764 FROM [ARABIDOPSIS THALIANA]DEACETYL VINDOLINE 4-O-ACETYLTRANSFERASE, GB:AAC9931; UNKNOWN PROTEIN SIMILAR TO UNKNOWN PROTEIN SIMILAR TO PUTATIVE | Transferases |
| 6238 | 837 | CARBOXYPHOSPHONOENOLPYRUVATE MUTASE, PUTATIVE SIMILAR TO CARBOXYPHOSPHONOENOLPYRUVATE MUTASE GI:47149 FROM [STREPTOMYCES HYGROSCOPICUS] | Mutase |
| 6242 | 838 | PEROXIDASE, PUTATIVE SIMILAR TO PEROXIDASE GI:1161565 FROM [LYCOPERSICON ESCULENTUM] | Oxidase |
| 6243 | 839 | AUXIN TRANSPORT PROTEIN EIR1, PUTATIVE SIMILAR TO AUXIN TRANSPORT PROTEIN EIR1 GI:3377507 FROM [ARABIDOPSIS THALIANA] | Transporter |

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| 6259 | 840 | RECEPTOR-LIKE PROTEIN KINASE GI:7529754 FROM [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN SIMILAR TO] | Kinase, Protein |
| 6264 | 841 | 1-AMINOCYCLOPROPANE-1-CARBOXYLATE OXIDASE, PUTATIVE SIMILAR TO 1-AMINOCYCLOPROPANE-1-CARBOXYLATE OXIDASE GI:3386565 FROM [SORGHUM BICOLOR] | Oxidase |
| 6269 | 842 | AMINO ACID CARRIER, PUTATIVE SIMILAR TO AMINO ACID CARRIER GI:3293031 FROM [RICINUS COMMUNIS] | Transporter |
| 6274 | 843 | LYSOPHOSPHOLIPASE ISOLOG, PUTATIVE SIMILAR TO LYSOPHOSPHOLIPASE ISOLOG GI:1931639 FROM [ARABIDOPSIS THALIANA] | Lipase |
| 6279 | 844 | ASPARTIC PROTEASE, NUCELLIN-LIKE PROTEIN SIMILAR TO NUCELLIN GB:AAB96882 [HORDEUM VULGARE] (NUCELLIN: SIMILAR TO ASPARTIC PROTEASE AND ITS SPECIFIC EXPRESSION IN NUCELLAR CELLS DURING DEGENERATION) | Protease |
| 6280 | 845 | ASCORBATE PEROXIDASE IDENTICAL TO THYLAKOID-BOUND ASCORBATE PEROXIDASE GB:CAA67426 [ARABIDOPSIS THALIANA] THYLAKOID-BOUND | Oxidase |
| 6283 | 846 | CAFFEIC ACID 3-O-METHYLTRANSFERASE SIMILAR TO CAFFEIC ACID 3-O-METHYLTRANSFERASE GB:O23760 [CLARKIA BREWERI][PUTATIVE] | Transferases |
| 6284 | 847 | CAFFEIC ACID 3-O-METHYLTRANSFERASE SIMILAR TO CAFFEIC ACID 3-O-METHYLTRANSFERASE GB:O23760 [CLARKIA BREWERI][PUTATIVE] | Transferases |
| 6299 | 848 | AUX1-LIKE PERMEASE SIMILAR TO AUX1 (REGULATOR OF ROOT GRAVITROPISM, PUTATIVE PERMEASE) GB:CAA67308 [ARABIDOPSIS THALIANA][PUTATIVE] | Transporter |
| 6308 | 849 | ENDO-1,3-BETA-GLUCANASE SIMILAR TO ENDO-1,3-BETA-GLUCANASE GB:BAA21110 [GOSSYPIMUM HIRSUTUM][PUTATIVE] | Glycosylase |
| 6309 | 850 | ENDO-1,3-BETA-GLUCANASE SIMILAR TO ENDO-1,3-BETA-GLUCANASE GB:BAA21110 [GOSSYPIMUM HIRSUTUM][PUTATIVE] | Glycosylase |

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| 6312 | 851 | REVERSE TRANSCRIPTASE GI:976278 FROM [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN CONTAINS SIMILARITY TO] | Transcriptase |
| 6321 | 852 | NADH DEHYDROGENASE SUBUNIT I[HYPOTHETICAL PROTEIN CONTAINS SIMILARITY TO] | Dehydrogenase |
| 6335 | 853 | PHOSPHOGLYCERATE MUTASE, PUTATIVE SIMILAR TO PHOSPHOGLYCERATE MUTASE GI:8979237 FROM [CHLAMYDIA MURIDARUM] | Mutase |
| 6336 | 854 | XYLOSIDASE, PUTATIVE SIMILAR TO XYLOSIDASE GI:2102655 FROM [ASPERGILLUS NIGER] | Glycosylase |
| 6339 | 855 | TREHALOSE-6-PHOSPHATE PHOSPHATASE (ATTPPB) IDENTICAL TO TREHALOSE-6-PHOSPHATE PHOSPHATASE (ATTPPB) GB:AF007779 [ARABIDOPSIS THALIANA] (TREHALOSE SYNTHESIS, A COMMON DISACCHARIDE THAT APPEARS TO PLAY A MAJOR ROLE IN DESICCATION TOLERANCE, PLANT J 1998 MAR;13(5):673-83) | Phosphatase |
| 6344 | 856 | TRANSPORTER CONTAINS PFAM PROFILE: PF00083 SUGAR (AND OTHER) TRANSPORTER[PUTATIVE] | Transporter |
| 6351 | 857 | PROTEIN PHOSPHATASE 2C SIMILAR TO PROTEIN PHOSPHATASE 2C GB:CAA72341 [MEDICAGO SATIVA]; CONTAINS PFAM PROFILE: PF00481 PROTEIN PHOSPHATASE 2C[PUTATIVE] | Phosphatase |
| 6355 | 858 | METHYLTRANSFERASE GB:AAD17428 [ARABIDOPSIS THALIANA]; UNKNOWN PROTEIN, 5' PARTIAL SIMILAR TO PUTATIVE | Transferases |
| 6357 | 859 | UDP-GLUCOSE GLUCOSYLTRANSFERASE, PUTATIVE SIMILAR TO UDP-GLUCOSE GLUCOSYLTRANSFERASE GI:3928543 FROM [ARABIDOPSIS THALIANA] | Transferases |
| 6362 | 860 | GLUTATHIONE TRANSFERASE, PUTATIVE SIMILAR TO GLUTATHIONE TRANSFERASE GI:2853219 FROM [CARICA PAPAYA] | Transferases |
| 6363 | 861 | GLUTATHIONE TRANSFERASE, PUTATIVE SIMILAR TO GLUTATHIONE TRANSFERASE GI:2853219 FROM [CARICA PAPAYA] | Transferases |

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| 6364 | 862 | GLUTATHIONE TRANSFERASE, PUTATIVE SIMILAR TO GLUTATHIONE TRANSFERASE GI:2853219 FROM [CARICA PAPAYA] | Transferases |
| 6365 | 863 | GLUTATHIONE S-TRANSFERASE, PUTATIVE SIMILAR TO 2,4-D INDUCIBLE GLUTATHIONE S-TRANSFERASE GI:2920666 FROM [GLYCINE MAX] | Transferases |
| 6366 | 864 | GLUTATHIONE TRANSFERASE, PUTATIVE SIMILAR TO GLUTATHIONE TRANSFERASE GI:2853219 FROM [CARICA PAPAYA] | Transferases |
| 6368 | 865 | EXOPOLYGALACTURONASE, PUTATIVE SIMILAR TO EXOPOLYGALACTURONASE GI:311962 FROM [ARABIDOPSIS THALIANA] | Glycosylase |
| 6372 | 866 | GIBBERELLIN 2- OXIDASE IDENTICAL TO GIBBERELLIN 2- OXIDASE GI:4678366 FROM [ARABIDOPSIS THALIANA] | Oxidase |
| 6376 | 867 | BETA-AMYRIN SYNTHASE, PUTATIVE SIMILAR TO BETA-AMYRIN SYNTHASE GI:3688600 FROM [PANAX GINSENG] | Synthase |
| 6380 | 868 | BETA-1,3-GLUCANASE, C TERMINAL FRAGMENT GI:2281103 FROM [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN SIMILAR TO][PUTATIVE] | Glycosylase |
| 6381 | 869 | RECEPTOR PROTEIN KINASE, PUTATIVE SIMILAR TO RECEPTOR PROTEIN KINASE GI:9280288 FROM [ARABIDOPSIS THALIANA] | Kinase, Protein |
| 6383 | 870 | FLAVANONE 3-HYDROXYLASE, PUTATIVE SIMILAR TO FLAVANONE 3-HYDROXYLASE GI:727410 FROM [PERSEA AMERICANA] | Hydroxylase |
| 6420 | 871 | INORGANIC PYROPHOSPHATASE IDENTICAL TO VACUOLAR-TYPE H ⁺ -TRANSLOCATING INORGANIC PYROPHOSPHATASE GI:6901678 FROM [ARABIDOPSIS THALIANA] | Phosphatase |
| 6426 | 872 | LEUCINE-RICH REPEAT TRANSMEMBRANE PROTEIN KINASE, PUTATIVE SIMILAR TO LEUCINE-RICH REPEAT TRANSMEMBRANE PROTEIN KINASE 2 GI:3360291 FROM [ZEA MAYS] | Kinase, Protein |

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| 6465 | 873 | NA+/H+ ANTIporter GI:4558666 FROM [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN SIMILAR TO][PUTATIVE] | Transporter |
| 6471 | 874 | ENT-KAURENE SYNTHASE, PUTATIVE SIMILAR TO ENT-KAURENE SYNTHASE GI:3056725 FROM [ARABIDOPSIS THALIANA] | Synthase |
| 6473 | 875 | BETA-1,3-GLUCANASE-LIKE PROTEIN GI:9758115 FROM [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN SIMILAR TO] | Glycosylase |
| 6475 | 876 | 2-DEHYDRO-3-DEOXYPHOSHOCTONATE ALDOLASE, PUTATIVE SIMILAR TO 2-DEHYDRO-3-DEOXYPHOSHOCTONATE ALDOLASE GI:1683630 FROM [MANNHEIMIA HAEMOLYTICA] | Aldolase |
| 6486 | 877 | NA+/H+ ANTIporter GI:1655701 FROM [XENOPUS LAEVIS][HYPOTHETICAL PROTEIN CONTAINS SIMILARITY TO] | Transporter |
| 6487 | 878 | RECEPTOR PROTEIN KINASE, PUTATIVE SIMILAR TO RECEPTOR PROTEIN KINASE GI:1389566 FROM [ARABIDOPSIS THALIANA] | Kinase, Protein |
| 6488 | 879 | PROTEIN PHOSPHATASE-2C, PUTATIVE SIMILAR TO PROTEIN PHOSPHATASE-2C GI:3643088 FROM [MESEMBRYANTHEMUM CRYSTALLINUM] | Phosphatase |
| 6492 | 880 | WALL-ASSOCIATED KINASE 4, PUTATIVE SIMILAR TO WALL-ASSOCIATED KINASE 4 GI:3355308 FROM [ARABIDOPSIS THALIANA] | Kinase, Protein |
| 6493 | 881 | WALL-ASSOCIATED KINASE 2, PUTATIVE SIMILAR TO WALL-ASSOCIATED KINASE 2 GI:4826399 FROM [ARABIDOPSIS THALIANA] | Kinase, Protein |
| 6532 | 882 | RECEPTOR PROTEIN KINASE, PUTATIVE SIMILAR TO RECEPTOR PROTEIN KINASE GI:1389566 FROM [ARABIDOPSIS THALIANA] | Kinase, Protein |
| 6538 | 883 | POLYGALACTURONASE, PUTATIVE SIMILAR TO POLYGALACTURONASE GI:7381227 FROM [LYCOPERSICON ESCULENTUM] | Glycosylase |
| 6541 | 884 | POLYGALACTURONASE, PUTATIVE SIMILAR TO POLYGALACTURONASE GI:7381227 FROM [LYCOPERSICON ESCULENTUM] | Glycosylase |

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| 6551 | 885 | ALPHA/BETA HYDROLASE FOLD | Hydrolase |
| 6554 | 886 | SULFATE TRANSPORTER CONTAINS PFAM PROFILE: PF00916 SULFATE TRANSPORTER FAMILY[PUTATIVE] | Transporter |
| 6555 | 887 | IRON/ASCORBATE OXIDOREDUCTASE FAMILY[PUTATIVE] | Reductase |
| 6556 | 888 | GIBBERELLIN 3 BETA-HYDROXYLASE SIMILAR TO GIBBERELLIN 3 BETA-HYDROXYLASE GB:AAC83647 [ARABIDOPSIS THALIANA][PUTATIVE] | Hydroxylase |
| 6557 | 889 | GIBBERELLIN 3 BETA-HYDROXYLASE IDENTICAL TO GIBBERELLIN 3 BETA-HYDROXYLASE GB:AAC83647 [ARABIDOPSIS THALIANA] | Hydroxylase |
| 6559 | 890 | ASPARTATE AMINOTRANSFERASE SIMILAR TO ASPARTATE AMINOTRANSFERASE B GB:Q06191 [SINORHIZOBIUM MELILOTI][PUTATIVE] | Transferases |
| 6573 | 891 | AMINO ACID TRANSPORTER PROTEIN DOMAIN | Transporter |
| 6586 | 892 | PROTEIN KINASE SIMILAR TO LEUCINE-RICH REPEAT TRANSMEMBRANE PROTEIN KINASE I GB:AAC27894 FROM [ZEA MAYS][PUTATIVE] | Kinase, Protein |
| 6604 | 893 | CINNAMOYL COA REDUCTASE, PUTATIVE SIMILAR TO CINNAMOYL COA REDUCTASE GB:AAF43141 GI:7239228 FROM [POPULUS TREMULOIDES] | Reductase |
| 6609 | 894 | PROTEIN KINASE, PUTATIVE SIMILAR TO RECEPTOR-LIKE SERINE/THREONINE KINASE GB:AAC50043 GI:2465923 FROM [ARABIDOPSIS THALIANA] | Kinase, Protein |
| 6633 | 895 | AMINO ACID PERMEASE IDENTICAL TO GP:AF019637[PUTATIVE] | Transporter |
| 6658 | 896 | AUXIN TRANSPORT PROTEIN IDENTICAL TO GPJ3785972 AC005560[PUTATIVE] | Transporter |
| 6663 | 897 | PROTEIN TRANSPORT PROTEIN SEC12P IDENTICAL TO GB:M95796, CONTAINS A WD-40 REPEAT DOMAIN[PUTATIVE] | Transporter |
| 6679 | 898 | BETA-1,3-GLUCANASE [PUTATIVE] | Glycosylase |
| 6699 | 899 | HISTIDINE KINASE [PUTATIVE] | Kinase, Protein |
| 6701 | 900 | XYLOGLUCAN-SPECIFIC GLUCANASE IDENTICAL TO GB:D63509[PUTATIVE] | Glycosylase |

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| 6704 | 901 | PURPLE ACID PHOSPHATASE CONTAINS METALLO-PHOSPHOESTERASE MOTIF (PS50185)[PUTATIVE] | Esterase |
| 6705 | 902 | PURPLE ACID PHOSPHATASE CONTAINS METALLO-PHOSPHOESTERASE MOTIF (PS50185)[PUTATIVE] | Esterase |
| 6711 | 903 | RECEPTOR PROTEIN KINASE SIMILAR TO BRASSINOSTEROID INSENSITIVE PROTEIN[PUTATIVE] | Kinase, Protein |
| 6714 | 904 | NA ⁺ /H ⁺ ANTIporter [PUTATIVE] | Transporter |
| 6716 | 905 | GLUTAMATE DECARBOXYLASE [PUTATIVE] | Decarboxylase |
| 6717 | 906 | GLUTAMATE DECARBOXYLASE [PUTATIVE] | Decarboxylase |
| 6737 | 907 | RECEPTOR-LIKE PROTEIN KINASE [PUTATIVE] | Kinase, Protein |
| 6752 | 908 | CINNAMOYL-COA REDUCTASE [PUTATIVE] | Reductase |
| 6759 | 909 | DNA POLYMERASE III GAMMA SUBUNIT [SIMILAR TO] | Polymerase |
| 6763 | 910 | NON-LTR RETROELEMENT REVERSE TRANSCRIPTASE [PUTATIVE] | Transcriptase |
| 6770 | 911 | TRANSPORT PROTEIN [PUTATIVE] | Transporter |
| 6775 | 912 | REVERSE TRANSCRIPTASE [PUTATIVE] | Transcriptase |
| 6781 | 913 | RECEPTOR-LIKE PROTEIN KINASE [PUTATIVE] | Kinase, Protein |
| 6782 | 914 | PECTATE LYASE [PUTATIVE] | Lyase |
| 6788 | 915 | RECEPTOR-LIKE PROTEIN KINASE [PUTATIVE] | Kinase, Protein |
| 6801 | 916 | GLUTATHIONE S-TRANSFERASE [PUTATIVE] | Transferases |
| 6806 | 917 | RIBONUCLEASE, RNS1 IDENTICAL TO GB:U05206; CONTAINS A RIBONUCLEASE T2 FAMILY HISTIDINE ACTIVE SITE SIGNATURE (PDOC00459)[PUTATIVE] | Nuclease |
| 6844 | 918 | HORMONE-RECEPTOR DOMAIN (PROSITE: QDOC50227) | Receptor |
| 6860 | 919 | ESTERASE (CONTAINS AN ESTERASE/LIPASE/THIOESTERASE ACTIVE SITE SERINE DOMAIN (PROSITE: PS50187); RELATED TO PLANT SENSITIVE RESPONSE PROTEINS[PUTATIVE] | Esterase |
| 6875 | 920 | URIDYLYL TRANSFERASE [PUTATIVE] | Transferases |
| 6877 | 921 | STEROID SULFOTRANSFERASE [PUTATIVE] | Transferases |
| 6878 | 922 | STEROID SULFOTRANSFERASE [PUTATIVE] | Transferases |

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| 6890 | 923 | LIPASE/HYDROLASE GDSL-motif SIMILAR TO APG PROTEINS; PFAM DOMAIN PF00657[PUTATIVE] | Lipase |
| 6892 | 924 | LIPASE/HYDROLASE GDSL-motif SIMILAR TO APG PROTEINS; PFAM DOMAIN PF00657[PUTATIVE] | Lipase |
| 6894 | 925 | IRON TRANSPORTER ROOT [PUTATIVE] | Transporter |
| 6908 | 926 | RIBONUCLEASE E [PUTATIVE] | Nuclease |
| 6910 | 927 | RECEPTOR-LIKE PROTEIN KINASE [PUTATIVE] | Kinase, Protein |
| 6920 | 928 | INDOLE-3-GLYCEROL PHOSPHATE SYNTHASE [PUTATIVE] | Synthase |
| 6922 | 929 | NON-LTR RETROELEMENT REVERSE TRANSCRIPTASE [PUTATIVE] | Transcriptase |
| 6933 | 930 | PROTEIN PHOSPHATASE [PUTATIVE] | Phosphatase |
| 6935 | 931 | LIPASE/HYDROLASE GDSL-motif SIMILAR TO APG PROTEINS; PFAM DOMAIN PF00657[PUTATIVE] | Lipase |
| 6936 | 932 | REVERSE TRANSCRIPTASE [PUTATIVE] | Transcriptase |
| 6946 | 933 | FERREDOXIN-THIOREDOXIN REDUCTASE [PUTATIVE] | Reductase |
| 6952 | 934 | NON-LTR RETROELEMENT REVERSE TRANSCRIPTASE [PUTATIVE] | Transcriptase |
| 6980 | 935 | PROTEIN KINASE CONTAINS A PROTEIN KINASE DOMAIN PROFILE (PDOC00100)[PUTATIVE] | Kinase, Protein |
| 6986 | 936 | PHOSPHORIBOSYLAMINOIMIDAZOLE CARBOXYLASE [PUTATIVE] | Carboxylase |
| 7023 | 937 | NON-LTR RETROELEMENT REVERSE TRANSCRIPTASE [PUTATIVE] | Transcriptase |
| 7038 | 938 | BETA-1,3-GLUCANASE [PUTATIVE] | Glycosylase |
| 7050 | 939 | SERINE PROTEASE [PUTATIVE] | Protease |
| 7057 | 940 | ENOYL-ACP REDUCTASE (ENR-A) IDENTICAL TO GB:Y13860 | Reductase |
| 7063 | 941 | 12-OXOPHYTODIENOATE-10,11-REDUCTASE | Reductase |
| 7110 | 942 | ENDOOXYLOGLUCAN GLYCOSYLTRANSFERASE IDENTICAL TO GB:D16454[PUTATIVE] | Transferases |
| 7115 | 943 | 1-AMINOCYCLOPROPANE-1-CARBOXYLATE OXIDASE | Oxidase |
| 7123 | 944 | RECEPTOR-LIKE PROTEIN KINASE [PUTATIVE] | Kinase, Protein |

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| 7125 | 945 | NON-LTR RETROELEMENT REVERSE TRANSCRIPTASE [PUTATIVE] | Transcriptase |
| 7126 | 946 | GAG-PROTEASE POLYPROTEIN POSSIBLE 3' PARTIAL[PUTATIVE] | Protease |
| 7133 | 947 | PROTEIN KINASE CONTAINS A PROTEIN KINASE DOMAIN PROFILE (PDOC00100)[PUTATIVE] | Kinase, Protein |
| 7168 | 948 | ABC TRANSPORTER [PUTATIVE] | Transporter |
| 7262 | 949 | MONOGALACTOSYLDIACYLGLYCEROL SYNTHASE [PUTATIVE] | Synthase |
| 7263 | 950 | REVERSE TRANSCRIPTASE TA1-1; GB:AAD17398[HYPOTHETICAL PROTEIN SIMILAR TO] | Transcriptase |
| 7295 | 951 | C-1-TETRAHYDROFOLATE SYNTHASE [PUTATIVE] | Synthase |
| 7331 | 952 | N-ACETYLGLUCOSAMINYLTRANSFERASE [PUTATIVE] | Transferases |
| 7352 | 953 | NA/H ANTIporter [PUTATIVE] | Transporter |
| 7365 | 954 | RECEPTOR-LIKE PROTEIN KINASE [PUTATIVE] | Kinase, Protein |
| 7366 | 955 | RECEPTOR-LIKE PROTEIN KINASE [PUTATIVE] | Kinase, Protein |
| 7367 | 956 | ASPARTATE AMINOTRANSFERASE [PUTATIVE] | Transferases |
| 7403 | 957 | PROLINE IMINOPEPTIDASE IDENTICAL TO GP:1710151:U72711 | Protease |
| 7404 | 958 | PROTEIN PHOSPHATASE 2C [PUTATIVE] | Phosphatase |
| 7436 | 959 | ENDOXYLOGLUCAN GLYCOSYLTRANSFERASE [PUTATIVE] | Transferases |
| 7441 | 960 | SUCROSE-PROTON SYMPORTER [PUTATIVE] | Transporter |
| 7443 | 961 | 1,4-BETA-XYLAN ENDOHYDROLASE | Hydrolase |
| 7446 | 962 | VACUOLAR SORTING RECEPTOR-LIKE PROTEIN | Receptor |
| 7448 | 963 | VACUOLAR SORTING RECEPTOR-LIKE PROTEIN | Receptor |
| 7465 | 964 | STEROID SULFOTRANSFERASE [PUTATIVE] | Transferases |
| 7500 | 965 | RECEPTOR-LIKE PROTEIN KINASE [PUTATIVE] | Kinase, Protein |
| 7504 | 966 | NON-LTR RETROELEMENT REVERSE TRANSCRIPTASE [PUTATIVE] | Transcriptase |
| 7509 | 967 | NON-LTR RETROELEMENT REVERSE TRANSCRIPTASE [PUTATIVE] | Transcriptase |

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| 7516 | 968 | POLYGALACTURONASE [PUTATIVE] | Glycosylase |
| 7517 | 969 | POLYGALACTURONASE [PUTATIVE] | Glycosylase |
| 7518 | 970 | POLYGALACTURONASE [PUTATIVE] | Glycosylase |
| 7519 | 971 | GLUCOSYLTRANSFERASE [PUTATIVE] | Transferases |
| 7520 | 972 | GLUCOSYLTRANSFERASE [PUTATIVE] | Transferases |
| 7522 | 973 | NON-LTR RETROELEMENT REVERSE TRANSCRIPTASE [PUTATIVE] | Transcriptase |
| 7533 | 974 | FERREDOXIN-NITRITE REDUCTASE | Reductase |
| 7543 | 975 | NON-LTR RETROELEMENT REVERSE TRANSCRIPTASE [PUTATIVE] | Transcriptase |
| 7546 | 976 | NON-LTR RETROELEMENT REVERSE TRANSCRIPTASE [PUTATIVE] | Transcriptase |
| 7550 | 977 | PEPTIDYL-PROLYL CIS-TRANS ISOMERASE CYCLOPHILIN-TYPE [PUTATIVE] | Isomerase |
| 7577 | 978 | NON-LTR RETROELEMENT REVERSE TRANSCRIPTASE [PUTATIVE] | Transcriptase |
| 7588 | 979 | BETA-1,3-ENDOGLUCANASE, 5' PARTIAL [PUTATIVE] | Glycosylase |
| 7589 | 980 | LRR RECEPTOR PROTEIN KINASE [PUTATIVE] | Kinase, Protein |
| 7592 | 981 | BETA-KETOACYL-COA SYNTHASE [PUTATIVE] | Synthase |
| 7604 | 982 | PURPLE ACID PHOSPHATASE PRECURSOR [PUTATIVE] | Phosphatase |
| 7612 | 983 | ARGININE DECARBOXYLASE IDENTICAL TO GP:1590814:U52851 | Decarboxylase |
| 7623 | 984 | PROTEIN KINASE CONTAINS A PROTEIN KINASE DOMAIN PROFILE (PDOC00100)[PUTATIVE] | Kinase, Protein |
| 7636 | 985 | PROTEIN KINASE CONTAINS A PROTEIN KINASE DOMAIN PROFILE (PDOC00100)[PUTATIVE] | Kinase, Protein |
| 7640 | 986 | GLUCONOKINASE [PUTATIVE] | Kinase |
| 7651 | 987 | GLUCOSYLTRANSFERASE [PUTATIVE] | Transferases |
| 7659 | 988 | TETRACYCLINE TRANSPORTER PROTEIN [PUTATIVE] | Transporter |
| 7660 | 989 | TETRACYCLINE TRANSPORTER PROTEIN [PUTATIVE] | Transporter |
| 7661 | 990 | TETRACYCLINE TRANSPORTER-LIKE PROTEIN, 3' PARTIAL IDENTICAL TO EGAD 110957 119053 | Transporter |
| 7664 | 991 | PROTEIN KINASE DOMAIN | Kinase, Protein |

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| 7685 | 992 | POLY(A) POLYMERASE [PUTATIVE] | Polymerase |
| 7688 | 993 | NON-LTR RETROELEMENT REVERSE TRANSCRIPTASE [PUTATIVE] | Transcriptase |
| 7691 | 994 | SERINE ACETYLTRANSFERASE (GB:AF112303) | Transferases |
| 7708 | 995 | SERINE PEPTIDASE RELATED TO THYMUS-SPECIFIC FROM HOMO SAPIENS | Protease |
| 7714 | 996 | PURPLE ACID PHOSPHATASE PRECURSOR [PUTATIVE] | Phosphatase |
| 7715 | 997 | PEROXIDASE [PUTATIVE] | Oxidase |
| 7716 | 998 | PEROXIDASE [PUTATIVE] | Oxidase |
| 7720 | 999 | AAA-TYPE ATPASE [PUTATIVE] | ATPase |
| 7724 | 1000 | INORGANIC PYROPHOSPHATASE [PUTATIVE] | Phosphatase |
| 7746 | 1001 | PROTEIN KINASE CONTAINS A PROTEIN KINASE DOMAIN PROFILE (PDOC00100)[PUTATIVE] | Kinase, Protein |
| 7752 | 1002 | PROTEIN KINASE CONTAINS A PROTEIN KINASE DOMAIN PROFILE (PDOC00100)[PUTATIVE] | Kinase, Protein |
| 7755 | 1003 | FLAVONOL 3-O-GLUCOSYLTRANSFERASE [PUTATIVE] | Transferases |
| 7756 | 1004 | FLAVONOL 3-O-GLUCOSYLTRANSFERASE [PUTATIVE] | Transferases |
| 7761 | 1005 | GERANYLGERANYL PYROPHOSPHATE SYNTHASE [PUTATIVE] | Synthase |
| 7763 | 1006 | GERANYLGERANYL PYROPHOSPHATE SYNTHASE CONTAINS GB:L22347[PUTATIVE] | Synthase |
| 7779 | 1007 | XYLOGLUCAN ENDO-TRANSGLYCOSYLASE [PUTATIVE] | Glycosylase |
| 7789 | 1008 | PROTEIN KINASE CONTAINS A PROTEIN KINASE DOMAIN PROFILE (PDOC00100)[PUTATIVE] | Kinase, Protein |
| 7798 | 1009 | PEROXIDASE (ATP22A) IDENTICAL TO GB:Y08781 | Oxidase |
| 7801 | 1010 | LIPASE/HYDROLASE GDSL-motif SIMILAR TO APG PROTEINS; PFAM DOMAIN PF00657[PUTATIVE] | Lipase |
| 7805 | 1011 | LIPASE/HYDROLASE GDSL-motif SIMILAR TO APG PROTEINS; PFAM DOMAIN PF00657[PUTATIVE] | Lipase |
| 7806 | 1012 | LIPASE/HYDROLASE GDSL-motif SIMILAR TO APG PROTEINS; PFAM DOMAIN PF00657[PUTATIVE] | Lipase |

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| 7807 | 1013 | ANTHRANILATE HYDROXYCINNAMOYL/BENZOYLTRANSFERASE [PUTATIVE] | N-Transferases |
| 7810 | 1014 | NON-LTR RETROELEMENT REVERSE TRANSCRIPTASE [PUTATIVE] | Transcriptase |
| 7813 | 1015 | RECEPTOR-LIKE PROTEIN KINASE [PUTATIVE] | Kinase, Protein |
| 7815 | 1016 | PECTINESTERASE [PUTATIVE] | Esterase |
| 7817 | 1017 | SERINE PROTEASE [PUTATIVE] | Protease |
| 7819 | 1018 | RECEPTOR-LIKE PROTEIN KINASE [PUTATIVE] | Kinase, Protein |
| 7821 | 1019 | RECEPTOR-LIKE PROTEIN KINASE [PUTATIVE] | Kinase, Protein |
| 7823 | 1020 | PROTEIN KINASE, 5'PARTIAL [PUTATIVE] | Kinase, Protein |
| 7844 | 1021 | BETA-1,3-ENDOGLUCANASE [PUTATIVE] | Glycosylase |
| 7850 | 1022 | CYTOKININ OXIDASE [PUTATIVE] | Oxidase |
| 7855 | 1023 | ALPHA/BETA HYDROLASE FOLD (PF00561).[PUTATIVE]; ESTERASE CONTAINS ESTERASE/LIPASE/THIOESTERASE ACTIVE SITE SERINE (PS50187) | Hydrolase |
| 7857 | 1024 | CYTIDINE DEAMINASE [PUTATIVE] | Deaminase |
| 7859 | 1025 | 1-AMINOCYCLOPROPANE-1-CARBOXYLATE OXIDASE | Oxidase |
| 7860 | 1026 | POTASSIUM/PROTON ANTIporter [PUTATIVE] | Transporter |
| 7894 | 1027 | N-ACETYL-GAMMA-GLUTAMYL-PHOSPHATE REDUCTASE [PUTATIVE] | Reductase |
| 7905 | 1028 | PROTEIN PHOSPHATASE 2C [PUTATIVE] | Phosphatase |
| 7930 | 1029 | PROTEIN KINASE CONTAINS A PROTEIN KINASE DOMAIN PROFILE (PDOC00100)[PUTATIVE] | Kinase, Protein |
| 7962 | 1030 | PROTEIN PHOSPHATASE 2C [PUTATIVE] | Phosphatase |
| 7969 | 1031 | (1-4)-BETA-MANNAN ENDOHYDROLASE | Hydrolase |
| 7970 | 1032 | RIBOFLAVIN SYNTHASE ALPHA CHAIN [PUTATIVE] | Synthase |
| 7985 | 1033 | SECRETORY CARRIER-ASSOCIATED MEMBRANE PROTEIN [PUTATIVE] | Transporter |
| 7986 | 1034 | LRR RECEPTOR PROTEIN KINASE [PUTATIVE] | Kinase, Protein |
| 8002 | 1035 | MAJOR INTRINSIC (CHANNEL) PROTEIN [PUTATIVE] | Channel |
| 8005 | 1036 | AUX1-LIKE AMINO ACID PERMEASE | Transporter |

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| 8016 | 1037 | SIGNAL SEQUENCE RECEPTOR, ALPHA SUBUNIT (SSR-ALPHA) SAME AS GP: 1174448[PUTATIVE] | Receptor |
| 8036 | 1038 | XYLULOSE KINASE [PUTATIVE] | Kinase |
| 8047 | 1039 | PROTEIN KINASE CONTAINS A PROTEIN KINASE DOMAIN PROFILE (PDOC00100)[PUTATIVE] | Kinase, Protein |
| 8054 | 1040 | DIHYDROFOLATE REDUCTASE, 3' PARTIAL [PUTATIVE] | Reductase |
| 8059 | 1041 | PECTINESTERASE [PUTATIVE] | Esterase |
| 8072 | 1042 | CELLULOSE SYNTHASE CATALYTIC SUBUNIT [PUTATIVE] | Synthase |
| 8084 | 1043 | CINNAMYL-ALCOHOL DEHYDROGENASE [PUTATIVE] | Dehydrogenases |
| 8089 | 1044 | SHIKIMATE KINASE PRECURSOR [PUTATIVE] | Kinase |
| 8113 | 1045 | TREHALOSE-6-PHOSPHATE PHOSPHATASE [PUTATIVE] | Phosphatase |
| 8115 | 1046 | BETA-HYDROXYACYL-ACP DEHYDRATASE [PUTATIVE] | Dehydratase |
| 8131 | 1047 | PEROXIDASE [PUTATIVE] | Oxidase |
| 8133 | 1048 | NON-LTR RETROELEMENT REVERSE TRANSCRIPTASE [PUTATIVE] | Transcriptase |
| 8134 | 1049 | GTP CYCLOHYDROLASE [PUTATIVE] | Hydrolase |
| 8137 | 1050 | PYROPHOSPHATE--FRUCTOSE-6-PHOSPHATE PHOSPHOTRANSFERASE [PUTATIVE] | 1-Transferases |
| 8147 | 1051 | ANTHOCYANIDIN-3-GLUCOSIDE RHAMNOSYLTRANSFERASE, 3' PARTIAL | Transferases |
| 8153 | 1052 | D-AMINO ACID DEHYDROGENASE [PUTATIVE] | Dehydrogenases |
| 8179 | 1053 | AMINO ACID ACETYLTRANSFERASE [PUTATIVE] | Transferases |
| 8181 | 1054 | FLAVONOL 3-O-GLUCOSYLTRANSFERASE [PUTATIVE] | Transferases |
| 8184 | 1055 | SERINE CARBOXYPEPTIDASE I, PSEUDOGENE SIMILAR TO SERINE CARBOXYPEPTIDASE I[PUTATIVE] | Protease |
| 8207 | 1056 | PROTEIN KINASE CONTAINS A PROTEIN KINASE DOMAIN PROFILE (PDOC00100)[PUTATIVE] | Kinase, Protein |
| 8208 | 1057 | GLUCOSYLTRANSFERASE [PUTATIVE] | Transferases |
| 8210 | 1058 | VETISPIRADIENE SYNTHASE [PUTATIVE] | Synthase |

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| 8212 | 1059 | GLUCOSYLTRANSFERASE [PUTATIVE] | Transferases |
| 8213 | 1060 | GLUCOSYLTRANSFERASE [PUTATIVE] | Transferases |
| 8217 | 1061 | RECEPTOR-LIKE PROTEIN KINASE [PUTATIVE] | Kinase, Protein |
| 8232 | 1062 | PROTEIN KINASE CONTAINS A PROTEIN KINASE DOMAIN PROFILE (PDOC00100)[PUTATIVE] | Kinase, Protein |
| 8238 | 1063 | ANTHRANILATE HYDROXYCINNAMOYL/BENZOYLTRANSFERASE [PUTATIVE] | N-Transferases |
| 8241 | 1064 | LIPASE/HYDROLASE GDSL-motif SIMILAR TO APG PROTEINS; PFAM DOMAIN PF00657[PUTATIVE] | Lipase |
| 8242 | 1065 | ACETONE-CYANOHYDRIN LYASE [PUTATIVE] | Lyase |
| 8243 | 1066 | ACETONE-CYANOHYDRIN LYASE [PUTATIVE] | Lyase |
| 8244 | 1067 | ACETONE-CYANOHYDRIN LYASE [PUTATIVE] | Lyase |
| 8245 | 1068 | ACETONE-CYANOHYDRIN LYASE [PUTATIVE] | Lyase |
| 8246 | 1069 | ACETONE-CYANOHYDRIN LYASE [PUTATIVE] | Lyase |
| 8247 | 1070 | ACETONE-CYANOHYDRIN LYASE [PUTATIVE] | Lyase |
| 8248 | 1071 | ACETONE-CYANOHYDRIN LYASE [PUTATIVE] | Lyase |
| 8249 | 1072 | ACETONE-CYANOHYDRIN LYASE [PUTATIVE] | Lyase |
| 8250 | 1073 | PECTINESTERASE [PUTATIVE] | Esterase |
| 8263 | 1074 | PROTEIN KINASE CONTAINS A PROTEIN KINASE DOMAIN PROFILE (PDOC00100)[PUTATIVE] | Kinase, Protein |
| 8266 | 1075 | GERANYLGERANYL PYROPHOSPHATE SYNTHASE IDENTICAL TO GB:U44876; SEQUENCE DISAGREES AT N-TERMINUS, SEQUENCE SUBMITTED HAS BEEN CONFIRMED FROM THREE ELECTROPHEROGRAMS. | Synthase |
| 8274 | 1076 | POLYGALACTURONASE [PUTATIVE] | Glycosylase |
| 8275 | 1077 | CINNAMOYL COA REDUCTASE [PUTATIVE] | Reductase |
| 8279 | 1078 | LRR RECEPTOR PROTEIN KINASE [PUTATIVE] | Kinase, Protein |
| 8282 | 1079 | CYCLIC NUCLEOTIDE AND CALMODULIN-REGULATED ION CHANNEL | Channel |
| 8296 | 1080 | RECEPTOR-LIKE PROTEIN KINASE [PUTATIVE] | Kinase, Protein |
| 8304 | 1081 | LIMONENE CYCLASE [PUTATIVE] | Cyclase |
| 8334 | 1082 | H ⁺ ATPASE, PLASMA MEMBRANE, 3' PARTIAL [PUTATIVE] | ATPase |

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| 8338 | 1083 | LIPASE/HYDROLASE GDSL-motif SIMILAR TO APG PROTEINS; PFAM DOMAIN PF00657[PUTATIVE] | Lipase |
| 8343 | 1084 | CYCLIC NUCLEOTIDE-REGULATED ION CHANNEL PROTEIN [PUTATIVE] | Channel |
| 8345 | 1085 | GLUCOSYLTRANSFERASE [PUTATIVE] | Transferases |
| 8353 | 1086 | LIGAND-GATED ION CHANNEL PROTEIN [PUTATIVE] | Channel |
| 8354 | 1087 | LIGAND-GATED ION CHANNEL PROTEIN [PUTATIVE] | Channel |
| 8358 | 1088 | PEROXIDASE [PUTATIVE] | Oxidase |
| 8399 | 1089 | PROTEIN KINASE DOMAIN | Kinase, Protein |
| 8420 | 1090 | DIOXYGENASE [PUTATIVE] | Oxygenases |
| 8429 | 1091 | CELLULOSE SYNTHASE CATALYTIC SUBUNIT [PUTATIVE] | Synthase |
| 8455 | 1092 | RECEPTOR-LIKE PROTEIN KINASE [PUTATIVE] | Kinase, Protein |
| 8498 | 1093 | BETA-KETOACYL-COA SYNTHASE (FIDDLEHEAD) IDENTICAL TO GB:AJ010713; CONTAINS A CHALCONE AND STILBENE SYNTHASE ACTIVE SITE (PF00195) | Synthase |
| 8502 | 1094 | PROTEIN KINASE CONTAINS A PROTEIN KINASE DOMAIN PROFILE (PDOC00100)[PUTATIVE] | Kinase, Protein |
| 8506 | 1095 | RECEPTOR-LIKE PROTEIN KINASE, ERECTA IDENTICAL TO GB:U47029 AND GB:D83257; CONTAINS A PROTEIN KINASE DOMAIN PROFILE (PDOC00100); CONTAINS LRR LEUCINE RICH REPEAT DOMAINS[PUTATIVE] | Kinase, Protein |
| 8509 | 1096 | MITOCHONDRIAL CARRIER PROTEIN [PUTATIVE] | Transporter |
| 8517 | 1097 | PECTINESTERASE [PUTATIVE] | Esterase |
| 8518 | 1098 | PECTINESTERASE [PUTATIVE] | Esterase |
| 8521 | 1099 | GLUCOSYLTRANSFERASE [PUTATIVE] | Transferases |
| 8526 | 1100 | PHEROMONE RECEPTOR AR781, SIMILAR TO YEAST; IDENTICAL TO GB:D88743, CORRECTED A FRAMESHIFT FOUND IN THE ORIGINAL RECORD (AT 69530 BP), SEQUENCE SUBMITTED HAS BEEN VERIFIED FROM 10 SEQUENCE ELECTROPHEROGRAMS. THE TRANSLATION NOW STARTS FROM AN UPSTREAM ATG. | Receptor |

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| 8528 | 1101 | HEME OXYGENASE 2 (HO2) | Oxygenases |
| 8533 | 1102 | BETA-1,3-GLUCANASE [PUTATIVE] | Glycosylase |
| 8535 | 1103 | POLYGALACTURONASE [PUTATIVE] | Glycosylase |
| 8537 | 1104 | BETA-KETOACYL-COA SYNTHASE [PUTATIVE] | Synthase |
| 8540 | 1105 | HEME OXYGENASE 1 (HO1) IDENTICAL TO GB:AF132475; ANNOTATION UPDATED PER SETH J. DAVIS AT UNIVERSITY OF WISCONSIN-MADISON | Oxygenases |
| 8546 | 1106 | RECEPTOR-LIKE PROTEIN KINASE [PUTATIVE] | Kinase, Protein |
| 8560 | 1107 | PHOSPHOLIPASE C [PUTATIVE] | Lipase |
| 8563 | 1108 | BILE ACID TRANSPORTER, NA ⁺ DEPENDENT ILEAL [PUTATIVE] | Transporter |
| 8579 | 1109 | RECEPTOR-LIKE PROTEIN KINASE [PUTATIVE] | Kinase, Protein |
| 8609 | 1110 | LIPASE [PUTATIVE] | Lipase |
| 8611 | 1111 | REVERSE TRANSCRIPTASE [PUTATIVE] | Transcriptase |
| 8624 | 1112 | BETA-1,3-GLUCANASE [PUTATIVE] | Glycosylase |
| 8630 | 1113 | FLAVONOL SULFOTRANSFERASE [PUTATIVE] | Transferases |
| 8655 | 1114 | PREPHENATE DEHYDRATASE/CHORISMATE MUTASE [PUTATIVE] | Dehydratase |
| 8658 | 1115 | DTDP-GLUCOSE 4-6-DEHYDRATASE [PUTATIVE] | Dehydratase |
| 8659 | 1116 | NON-LTR RETROELEMENT REVERSE TRANSCRIPTASE [PUTATIVE] | Transcriptase |
| 8680 | 1117 | GLUCOSYLTRANSFERASE [PUTATIVE] | Transferases |
| 8693 | 1118 | CARBONIC ANHYDRASE [PUTATIVE] | Anhydrase |
| 8697 | 1119 | PROTEIN KINASE CONTAINS A PROTEIN KINASE DOMAIN PROFILE (PDOC00100)[PUTATIVE] | Kinase, Protein |
| 8698 | 1120 | CYCLIC NUCLEOTIDE AND CALMODULIN-REGULATED ION CHANNEL PROTEIN [PUTATIVE] | Channel |
| 8719 | 1121 | PHEROMONE RECEPTOR DEFICIENT MUTANT [SIMILAR TO] | Receptor |
| 8758 | 1122 | PARA-AMINOBENZOATE SYNTHASE AND GLUTAMINE AMIDOTRANSFERASE, A BIFUNCTIONAL ENZYME [PUTATIVE] | Synthase |
| 8760 | 1123 | MEMBRANE CHANNEL PROTEIN [PUTATIVE] | Channel |

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| 8769 | 1124 | RECEPTOR-LIKE PROTEIN KINASE [PUTATIVE] | Kinase, Protein |
| 8778 | 1125 | LIGAND-GATED ION CHANNEL PROTEIN [PUTATIVE] | Channel |
| 8779 | 1126 | LIGAND-GATED ION CHANNEL PROTEIN [PUTATIVE] | Channel |
| 8780 | 1127 | LIGAND-GATED ION CHANNEL PROTEIN [PUTATIVE] | Channel |
| 8784 | 1128 | TROPINONE REDUCTASE [PUTATIVE] | Reductase |
| 8789 | 1129 | PROTEIN KINASE CONTAINS A PROTEIN KINASE DOMAIN PROFILE (PDOC00100)[PUTATIVE] | Kinase, Protein |
| 8792 | 1130 | PROTEIN KINASE CONTAINS A PROTEIN KINASE DOMAIN PROFILE (PDOC00100)[PUTATIVE] | Kinase, Protein |
| 8793 | 1131 | TROPINONE REDUCTASE [PUTATIVE] | Reductase |
| 8794 | 1132 | TROPINONE REDUCTASE [PUTATIVE] | Reductase |
| 8800 | 1133 | TROPINONE REDUCTASE [PUTATIVE] | Reductase |
| 8801 | 1134 | TROPINONE REDUCTASE [PUTATIVE] | Reductase |
| 8803 | 1135 | PROTEIN PHOSPHATASE 2C [PUTATIVE] | Phosphatase |
| 8807 | 1136 | GLUTATHIONE S-TRANSFERASE [PUTATIVE] | Transferases |
| 8809 | 1137 | GLUTATHIONE S-TRANSFERASE [PUTATIVE] | Transferases |
| 8810 | 1138 | GLUTATHIONE S-TRANSFERASE IDENTICAL TO GB:X89216 | Transferases |
| 8811 | 1139 | GLUTATHIONE S-TRANSFERASE [PUTATIVE] | Transferases |
| 8812 | 1140 | GLUTATHIONE S-TRANSFERASE [PUTATIVE] | Transferases |
| 8813 | 1141 | GLUTATHIONE S-TRANSFERASE [PUTATIVE] | Transferases |
| 8814 | 1142 | GLUTATHIONE S-TRANSFERASE [PUTATIVE] | Transferases |
| 8834 | 1143 | ANTHRANILATE SYNTHASE, ALPHA SUBUNIT IDENTICAL TO GB:M92354 | Synthase |
| 8836 | 1144 | FLAVONOL 3-O-GLUCOSYLTRANSFERASE [PUTATIVE] | Transferases |
| 8837 | 1145 | MONOOXYGENASE [PUTATIVE] | Oxygenases |
| 8838 | 1146 | FLAVONOL 3-O-GLUCOSYLTRANSFERASE [PUTATIVE] | Transferases |
| 8839 | 1147 | FLAVONOL 3-O-GLUCOSYLTRANSFERASE [PUTATIVE] | Transferases |
| 8840 | 1148 | FLAVONOL 3-O-GLUCOSYLTRANSFERASE [PUTATIVE] | Transferases |

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| 8864 | 1149 | NADH DEHYDROGENASE (UBIQUINONE OXIDOREDUCTASE) [PUTATIVE] | Dehydrogenase |
| 8872 | 1150 | HIGH-AFFINITY POTASSIUM TRANSPORTER (ATKUP1) IDENTICAL TO GB:AF029876 | Transporter |
| 8873 | 1151 | FE(II) TRANSPORT PROTEIN [PUTATIVE] | Transporter |
| 8879 | 1152 | GLUCOSYLTRANSFERASE [PUTATIVE] | Transferases |
| 8880 | 1153 | GLUCOSYLTRANSFERASE [PUTATIVE] | Transferases |
| 8885 | 1154 | LIPASE/HYDROLASE GDSL-motif SIMILAR TO APG PROTEINS; PFAM DOMAIN PF00657[PUTATIVE] | Lipase |
| 8887 | 1155 | NA/H ANTIporter [PUTATIVE] | Transporter |
| 8892 | 1156 | VACUOLAR SORTING RECEPTOR [PUTATIVE] | Receptor |
| 8894 | 1157 | LIPASE/HYDROLASE GDSL-motif SIMILAR TO APG PROTEINS; PFAM DOMAIN PF00657[PUTATIVE] | Lipase |
| 8895 | 1158 | PSEUDOURIDINE SYNTHASE [PUTATIVE] | Synthase |
| 8907 | 1159 | SIGNAL PEPTIDASE I [PUTATIVE] | Protease |
| 8917 | 1160 | LIPASE [PUTATIVE] | Lipase |
| 8929 | 1161 | TROPINONE REDUCTASE [PUTATIVE] | Reductase |
| 8935 | 1162 | PROTEIN KINASE CONTAINS A PROTEIN KINASE DOMAIN PROFILE (PDOC00100)[PUTATIVE] | Kinase, Protein |
| 8936 | 1163 | PROTEIN KINASE CONTAINS A PROTEIN KINASE DOMAIN PROFILE (PDOC00100)[PUTATIVE] | Kinase, Protein |
| 8945 | 1164 | DIOXYGENASE [PUTATIVE] | Oxygenases |
| 8946 | 1165 | DIOXYGENASE [PUTATIVE] | Oxygenases |
| 8947 | 1166 | GLUTATHIONE S-TRANSFERASE IDENTICAL TO GB:Y12295 | Transferases |
| 8948 | 1167 | GLUTATHIONE S-TRANSFERASE IDENTICAL TO GB:D17673 | Transferases |
| 8955 | 1168 | PROTEIN KINASE CONTAINS A PROTEIN KINASE DOMAIN PROFILE (PDOC00100)[PUTATIVE] | Kinase, Protein |
| 8972 | 1169 | LIPASE [PUTATIVE] | Lipase |
| 8987 | 1170 | GLUTAMYL TRNA REDUCTASE [PUTATIVE] | Reductase |
| 8998 | 1171 | DELTA 9 DESATURASE ALMOST IDENTICAL (4 AA DIFFT) TO GP:2970036 | Desaturases |
| 9001 | 1172 | FRUCTOKINASE [PUTATIVE] | Kinase |

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| 9016 | 1173 | LIPASE/HYDROLASE GDSL-motif SIMILAR TO APG PROTEINS; PFAM DOMAIN PF00657[PUTATIVE] | Lipase |
| 9017 | 1174 | LIPASE/HYDROLASE GDSL-motif SIMILAR TO APG PROTEINS; PFAM DOMAIN PF00657[PUTATIVE] | Lipase |
| 9031 | 1175 | TRIACYLGLYCEROL LIPASE [PUTATIVE] | Lipase |
| 9038 | 1176 | GLUCOSYLTRANSFERASE [PUTATIVE] | Transferases |
| 9042 | 1177 | GLUCOSYLTRANSFERASE [PUTATIVE] | Transferases |
| 9043 | 1178 | PROTEIN KINASE CONTAINS A PROTEIN KINASE DOMAIN PROFILE (PDOC00100)[PUTATIVE] | Kinase, Protein |
| 9044 | 1179 | ACETOLACTATE SYNTHASE [PUTATIVE] | Synthase |
| 9054 | 1180 | NA ⁺ /H ⁺ ANTIporter [PUTATIVE] | Transporter |
| 9060 | 1181 | GLUCAN SYNTHASE [PUTATIVE] | Synthase |
| 9066 | 1182 | ALANINE ACETYL TRANSFERASE [PUTATIVE] | Transferases |
| 9067 | 1183 | ALANINE ACETYL TRANSFERASE [PUTATIVE] | Transferases |
| 9078 | 1184 | HYDROLASE [PUTATIVE] | Hydrolase |
| 9090 | 1185 | FE(II) TRANSPORTER IDENTICAL TO GB:AF033537[PUTATIVE] | Transporter |
| 9092 | 1186 | BETA-AMYLASE [PUTATIVE] | Glycosylase |
| 9108 | 1187 | O-GLCNAC TRANSFERASE [PUTATIVE] | Transferases |
| 9116 | 1188 | CELLULOSE SYNTHASE [PUTATIVE] | Synthase |
| 9117 | 1189 | CELLULOSE SYNTHASE [PUTATIVE] | Synthase |
| 9124 | 1190 | CELLULOSE SYNTHASE [PUTATIVE] | Synthase |
| 9125 | 1191 | CELLULOSE SYNTHASE [PUTATIVE] | Synthase |
| 9140 | 1192 | PURPLE ACID PHOSPHATASE PRECURSOR [PUTATIVE] | Phosphatase |
| 9143 | 1193 | PROTEIN KINASE CONTAINS A PROTEIN KINASE DOMAIN PROFILE (PDOC00100)[PUTATIVE] | Kinase, Protein |
| 9146 | 1194 | PHOSPHATE TRANSPORTER [PUTATIVE] | Transporter |
| 9173 | 1195 | CELLULOSE SYNTHASE [PUTATIVE] | Synthase |
| 9178 | 1196 | POLYGALACTURONASE [PUTATIVE] | Glycosylase |
| 9179 | 1197 | RECEPTOR-LIKE PROTEIN KINASE [PUTATIVE] | Kinase, Protein |
| 9185 | 1198 | FLAVIN-CONTAINING MONOOXYGENASE [PUTATIVE] | Oxygenases |
| 9188 | 1199 | TYROSINE-SPECIFIC TRANSPORT PROTEIN [PUTATIVE] | Transporter |

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| 9220 | 1200 | PROTEIN KINASE CONTAINS A PROTEIN KINASE DOMAIN PROFILE (PDOC00100)[PUTATIVE] | Kinase, Protein |
| 9221 | 1201 | CINNAMOYL-COA REDUCTASE HIGHLY SIMILAR TO F4P9.37[PUTATIVE] | Reductase |
| 9222 | 1202 | CINNAMOYL-COA REDUCTASE HIGHLY SIMILAR TO F4P9.36[PUTATIVE] | Reductase |
| 9242 | 1203 | MITOCHONDRIAL CARRIER PROTEIN [PUTATIVE] | Transporter |
| 9257 | 1204 | PEROXIDASE [PUTATIVE] | Oxidase |
| 9280 | 1205 | PROTEIN KINASE CONTAINS A PROTEIN KINASE DOMAIN PROFILE (PDOC00100)[PUTATIVE] | Kinase, Protein |
| 9283 | 1206 | NON-LTR RETROELEMENT REVERSE TRANSCRIPTASE [PUTATIVE] | Transcriptase |
| 9306 | 1207 | GIBBERELLIN 2-OXIDASE [PUTATIVE] | Oxidase |
| 9325 | 1208 | PROTEIN PHOSPHATASE 2C [PUTATIVE] | Phosphatase |
| 9344 | 1209 | VACUOLAR SORTING RECEPTOR [PUTATIVE] | Receptor |
| 9347 | 1210 | PHOSPHATIDYLINOSITOL-GLYCAN SYNTHASE [PUTATIVE] | Synthase |
| 9355 | 1211 | POTASSIUM TRANSPORTER [PUTATIVE] | Transporter |
| 9385 | 1212 | PEROXIDASE [PUTATIVE] | Oxidase |
| 9409 | 1213 | RECEPTOR-LIKE PROTEIN KINASE [PUTATIVE] | Kinase, Protein |
| 9412 | 1214 | GLUCOSYLTRANSFERASE [PUTATIVE] | Transferases |
| 9413 | 1215 | MONOOXYGENASE [PUTATIVE] | Oxygenases |
| 9428 | 1216 | MITOCHONDRIAL CARRIER PROTEIN [PUTATIVE] | Transporter |
| 9469 | 1217 | PHOSPHORIBOSYLFORMIMINO-5-AMINOIMIDAZOLE CARBOXAMIDE RIBOTIDE ISOMERASE IDENTICAL TO AB006139 | Isomerase |
| 9500 | 1218 | RECEPTOR-LIKE PROTEIN KINASE [PUTATIVE] | Kinase, Protein |
| 9502 | 1219 | PROLINE TRANSPORTER [PUTATIVE] | Transporter |
| 9509 | 1220 | ASPARTYL PROTEASE FAMILY (PF00026)[PUTATIVE] | Protease |
| 9511 | 1221 | GIBERELLIN BETA-HYDROXYLASE CONTAINS SIMILARITIES TO GA BETA-20-HYDROXYLASE FROM TOBACCO (GB:3327245) AND TO ETHYLENE FORMING ENZYME FROM PICEA GLAUCA (GB:L42466)[PUTATIVE] | Hydroxylase |

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| 9512 | 1222 | PECTINESTERASE [PUTATIVE] | Esterase |
| 9513 | 1223 | PECTINESTERASE [PUTATIVE] | Esterase |
| 9517 | 1224 | GLUCOSYL TRANSFERASE [PUTATIVE] | Transferases |
| 9518 | 1225 | GLUCOSYL TRANSFERASE [PUTATIVE] | Transferases |
| 9519 | 1226 | GLUCOSYL TRANSFERASE [PUTATIVE] | Transferases |
| 9520 | 1227 | GLUCOSYL TRANSFERASE [PUTATIVE] | Transferases |
| 9521 | 1228 | GLUCOSYL TRANSFERASE AN EST MATCHING THE 5' END OF THIS GENE (GB:AA605508) WAS ORIGINALLY DESCRIBED AS POLYADENYLATED (GB:AA006321) AND IS PROBABLY TRANSCRIBED FROM THE OPPOSITE STRAND[PUTATIVE] | Transferases |
| 9522 | 1229 | GLUCOSYL TRANSFERASE [PUTATIVE] | Transferases |
| 9527 | 1230 | GLUCAN SYNTHASE [PUTATIVE] | Synthase |
| 9528 | 1231 | XYLOGLUCAN ENDO-TRANSGLYCOSYLASE [PUTATIVE] | Glycosylase |
| 9538 | 1232 | GLUCOSYLTRANSFERASE [PUTATIVE] | Transferases |
| 9540 | 1233 | RNA POLYMERASE SIGMA-70 FACTOR [PUTATIVE] | Polymerase |
| 9546 | 1234 | RECEPTOR-LIKE PROTEIN KINASE [PUTATIVE] | Kinase, Protein |
| 9554 | 1235 | PEROXIDASE ATP2A [PUTATIVE] | Oxidase |
| 9555 | 1236 | VETISPIRADIENE SYNTHASE [PUTATIVE] | Synthase |
| 9591 | 1237 | GLUTAMATE/ORNITHINE ACETYLTRANSFERASE [PUTATIVE] | Transferases |
| 9611 | 1238 | PHOSPHORIBOSYLAMINOIMIDAZOLE CARBOXYLASE [PUTATIVE] | Carboxylase |
| 9612 | 1239 | CER1-LIKE PROTEIN MAY BE INVOLVED IN WAX BIOSYNTHESIS; CONTAINS A SUR2-TYPE HYDROXYLASE/DESATURASE CATALYTIC DOMAIN (PS50242) | Desaturases |
| 9613 | 1240 | RECEPTOR-LIKE PROTEIN KINASE SAME AS GB:X95909 (POLYMORPHISM EXISTS AT A GA REPEAT. WE FOUND 6 COPIES IN OUR SEQUENCE WHEREAS ONLY 5 COPIES EXIST IN GB:X95909)[PUTATIVE] | Kinase, Protein |

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| 9645 | 1241 | ALPHA-CARBOXYLTRANSFERASE [PUTATIVE] | Transferases |
| 9651 | 1242 | PEPTIDE/AMINO ACID TRANSPORTER [PUTATIVE] | Transporter |
| 9658 | 1243 | HIGH AFFINITY CA ²⁺ ANTIporter IDENTICAL TO GB:U57411, EXCEPT A POSSIBLE FRAMESHIFT AT BASE 58008. SEQUENCE HAS BEEN CONFIRMED WITH 5 SEQUENCING READS. | Transporter |
| 9665 | 1244 | ANTHOCYANIDIN SYNTHASE [PUTATIVE] | Synthase |
| 9669 | 1245 | AMMONIUM TRANSPORTER [PUTATIVE] | Transporter |
| 9678 | 1246 | PEROXIDASE IDENTICAL TO M58381 | Oxidase |
| 9679 | 1247 | PEROXIDASE | Oxidase |
| 9700 | 1248 | ACID PHOSPHATASE CONTAINS METALLO-PHOSPHOESTERASE MOTIF (PS50185)[PUTATIVE] | Esterase |
| 9734 | 1249 | PHOSPHATE TRANSPORTER (ATPT2) IDENTICAL TO GB:U62331 | Transporter |
| 9743 | 1250 | PEROXIDASE [PUTATIVE] | Oxidase |
| 9750 | 1251 | PROTEIN KINASE CONTAINS A PROTEIN KINASE DOMAIN PROFILE (PDOC00100)[PUTATIVE] | Kinase, Protein |
| 9757 | 1252 | PROTEIN KINASE CONTAINS A PROTEIN KINASE DOMAIN PROFILE (PDOC00100)[PUTATIVE] | Kinase, Protein |
| 9758 | 1253 | ABC TRANSPORTER [PUTATIVE] | Transporter |
| 9766 | 1254 | ADENYLATE KINASE [PUTATIVE] | Kinase |
| 9768 | 1255 | CDP-DIACYLGLYCEROL--GLYCEROL-3-PHOSPHATE 3-PHOSPHATIDYLTRANSFERASE [PUTATIVE] | Transferases |
| 9775 | 1256 | PROTEIN KINASE CONTAINS A PROTEIN KINASE DOMAIN PROFILE (PDOC00100)[PUTATIVE] | Kinase, Protein |
| 9779 | 1257 | PHOSPHOLIPASE [PUTATIVE] | Lipase |
| 9780 | 1258 | PHOSPHOLIPASE [PUTATIVE] | Lipase |
| 9781 | 1259 | PHOSPHOLIPASE [PUTATIVE] | Lipase |
| 9801 | 1260 | BETA-1,3-ENDOGLUCANASE [PUTATIVE] | Glycosylase |
| 9803 | 1261 | PROTEIN KINASE [PUTATIVE] | Kinase, Protein |
| 9815 | 1262 | RIBONUCLEASE, RNS2 IDENTICAL TO SP:P42814:RNS2_ARATH; CONTAINS A RIBONUCLEASE T2 FAMILY HISTIDINE ACTIVE SITE SIGNATURE (PDOC00459)[PUTATIVE] | Nuclease |
| 9822 | 1263 | SERINE PROTEASE [PUTATIVE] | Protease |

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| 9825 | 1264 | PROLINE TRANSPORTER 1 | Transporter |
| 9829 | 1265 | ISOAMYLASE [PUTATIVE] | Glycosylase |
| 9834 | 1266 | ANTHOCYANIN 5-AROMATIC ACYLTRANSFERASE [PUTATIVE] | Transferases |
| 9859 | 1267 | ANTHRANILATE HYDROXYCINNAMOYL/BENZOYLTRANSFERASE [PUTATIVE] | N-Transferases |
| 9861 | 1268 | LIPASE/HYDROLASE GDSL-motif SIMILAR TO APG PROTEINS; PFAM DOMAIN PF00657[PUTATIVE] | Lipase |
| 9863 | 1269 | PROTEIN KINASE CONTAINS A PROTEIN KINASE DOMAIN PROFILE (PDOC00100)[PUTATIVE] | Kinase, Protein |
| 9867 | 1270 | POLYGALACTURONASE [PUTATIVE] | Glycosylase |
| 9890 | 1271 | PROTEIN KINASE CONTAINS A PROTEIN KINASE DOMAIN PROFILE (PDOC00100)[PUTATIVE] | Kinase, Protein |
| 9894 | 1272 | POTASSIUM TRANSPORTER [PUTATIVE] | Transporter |
| 9896 | 1273 | PROTEIN KINASE CONTAINS A PROTEIN KINASE DOMAIN PROFILE (PDOC00100)[PUTATIVE] | Kinase, Protein |
| 9897 | 1274 | INITIATOR TRNA PHOSPHORIBOSYL-TRANSFERASE [PUTATIVE] | Transferases |
| 9898 | 1275 | PROTEIN KINASE CONTAINS A PROTEIN KINASE DOMAIN PROFILE (PDOC00100)[PUTATIVE] | Kinase, Protein |
| 9908 | 1276 | NON-LTR RETROELEMENT REVERSE TRANSCRIPTASE [PUTATIVE] | Transcriptase |
| 9909 | 1277 | GLYCEROL-3-PHOSPHATE DEHYDROGENASE | Dehydrogenases |
| 9927 | 1278 | PROTEIN KINASE CONTAINS A PROTEIN KINASE DOMAIN PROFILE (PDOC00100)[PUTATIVE] | Kinase, Protein |
| 9963 | 1279 | GLUTAMATE SYNTHASE FERRODOXIN-DEPENDENT , 3' PARTIAL [PUTATIVE] | Synthase |
| 9973 | 1280 | DNA-DIRECTED RNA POLYMERASE 23KD SUBUNIT [PUTATIVE] | Polymerase |
| 9987 | 1281 | PEROXIDASE [PUTATIVE] | Oxidase |
| 9990 | 1282 | CYTOKININ OXIDASE [PUTATIVE] | Oxidase |
| 9993 | 1283 | GLYCEROL-3-PHOSPHATE DEHYDROGENASE | Dehydrogenases |

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| 10007 | 1284 | THIOREDOXIN REDUCTASE THE LAST 2 EXONS ENCODE THIOREDOXIN. THERE IS AN EST MATCH TO EXONS 5-7, AND THE DISTANCE BETWEEN EXON 7 AND EXON 8 IS ONLY 90BP. IT IS UNLIKELY THIS IS TWO SEPARATE GENES, BUT MORE LIKELY A HYBRID PROTEIN.[PUTATIVE] | Reductase |
| 10021 | 1285 | RECEPTOR-LIKE PROTEIN KINASE [PUTATIVE] | Kinase, Protein |
| 10024 | 1286 | POLYGALACTURONASE [PUTATIVE] | Glycosylase |
| 10028 | 1287 | RECEPTOR-LIKE PROTEIN KINASE [PUTATIVE] | Kinase, Protein |
| 10030 | 1288 | PROTEIN KINASE CONTAINS A PROTEIN KINASE DOMAIN PROFILE (PDOC00100)[PUTATIVE] | Kinase, Protein |
| 10031 | 1289 | PROTEIN KINASE CONTAINS A PROTEIN KINASE DOMAIN PROFILE (PDOC00100)[PUTATIVE] | Kinase, Protein |
| 10032 | 1290 | PROTEIN KINASE CONTAINS A PROTEIN KINASE DOMAIN PROFILE (PDOC00100)[PUTATIVE] | Kinase, Protein |
| 10040 | 1291 | PHOSPHOLIPASE D | Lipase |
| 10066 | 1292 | PROTEIN KINASE, 5' PARTIAL [PUTATIVE] | Kinase, Protein |
| 10085 | 1293 | COPPER AMINE OXIDASE [PUTATIVE] | Oxidase |
| 10096 | 1294 | PHOSPHOENOLPYRUVATE CARBOXYLASE | Carboxylase |
| 10105 | 1295 | LIPASE [PUTATIVE] | Lipase |
| 10115 | 1296 | CITRATE SYNTHASE [PUTATIVE] | Synthase |
| 10127 | 1297 | RIBOSE PHOSPHATE PYROPHOSPHOKINASE [PUTATIVE] | Kinase |
| 10133 | 1298 | PROTEIN KINASE CONTAINS A PROTEIN KINASE DOMAIN PROFILE (PDOC00100)[PUTATIVE] | Kinase, Protein |
| 10141 | 1299 | PECTINESTERASE [PUTATIVE] | Esterase |
| 10145 | 1300 | ISOPROPYLMALATE DEHYDRATASE [PUTATIVE] | Dehydratase |
| 10146 | 1301 | ISOPROPYLMALATE DEHYDRATASE | Dehydratase |
| 10151 | 1302 | 3-ISOPROPYLMALATE DEHYDRATASE, SMALL SUBUNIT | Dehydratase |
| 10152 | 1303 | 3-ISOPROPYLMALATE DEHYDRATASE, SMALL SUBUNIT | Dehydratase |
| 10160 | 1304 | CARBOXYPHOSPHOENOLPYRUVATE MUTASE [PUTATIVE] | Mutase |

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| 10165 | 1305 | PROTEIN KINASE CONTAINS A PROTEIN KINASE DOMAIN PROFILE (PDOC00100)[PUTATIVE] | Kinase, Protein |
| 10177 | 1306 | BIOTIN SYNTHASE (BIO B) | Synthase |
| 10189 | 1307 | PEROXIDASE [PUTATIVE] | Oxidase |
| 10197 | 1308 | PEPTIDYL-PROLYL CIS-TRANS ISOMERASE FKBP TYPE [PUTATIVE] | Isomerase |
| 10198 | 1309 | ENDOCHITINASE [PUTATIVE] | Chitinase |
| 10199 | 1310 | ENDOCHITINASE [PUTATIVE] | Chitinase |
| 10200 | 1311 | ENDOCHITINASE [PUTATIVE] | Chitinase |
| 10201 | 1312 | ENDOCHITINASE [PUTATIVE] | Chitinase |
| 10202 | 1313 | ENDOCHITINASE [PUTATIVE] | Chitinase |
| 10203 | 1314 | ENDOCHITINASE [PUTATIVE] | Chitinase |
| 10207 | 1315 | BETA-1,3-GLUCANASE, C TERMINAL FRAGMENT C TERMINAL HOMOLGY ONLY[PUTATIVE] | Glycosylase |
| 10208 | 1316 | BETA-1,3-GLUCANASE, C TERMINAL FRAGMENT C TERMINAL HOMOLGY ONLY[PUTATIVE] | Glycosylase |
| 10210 | 1317 | RECEPTOR PROTEIN KINASE [PUTATIVE] | Kinase, Protein |
| 10211 | 1318 | RECEPTOR PROTEIN KINASE [PUTATIVE] | Kinase, Protein |
| 10212 | 1319 | STEAROYL-ACP DESATURASE | Desaturases |
| 10223 | 1320 | GLUCOSYLTRANSFERASE [PUTATIVE] | Transferases |
| 10224 | 1321 | PROTEIN KINASE CONTAINS A PROTEIN KINASE DOMAIN PROFILE (PDOC00100)[PUTATIVE] | Kinase, Protein |
| 10225 | 1322 | GLUCOSYLTRANSFERASE [PUTATIVE] | Transferases |
| 10226 | 1323 | PROTEIN KINASE CONTAINS A PROTEIN KINASE DOMAIN PROFILE (PDOC00100)[PUTATIVE] | Kinase, Protein |
| 10227 | 1324 | POLYGALACTURONASE [PUTATIVE] | Glycosylase |
| 10228 | 1325 | POLYGALACTURONASE [PUTATIVE] | Glycosylase |
| 10229 | 1326 | POLYGALACTURONASE ISOLOG, 3' PARTIAL | Glycosylase |
| 10230 | 1327 | POLYGALACTURONASE [PUTATIVE] | Glycosylase |
| 10232 | 1328 | METHYL CHLORIDE TRANSFERASE [PUTATIVE] | Transferases |
| 10234 | 1329 | PROTEIN KINASE CONTAINS A PROTEIN KINASE DOMAIN PROFILE (PDOC00100)[PUTATIVE] | Kinase, Protein |
| 10246 | 1330 | 6,7-DIMETHYL-8-RIBITYLLUMAZINE SYNTHASE PRECURSOR | Synthase |

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| 10293 | 1331 | HEME A: FARNESYLTRANSFERASE [PUTATIVE] | Transferases |
| 10320 | 1332 | FLAVONOL SYNTHASE [PUTATIVE] | Synthase |
| 10321 | 1333 | TRIACYLGLYCEROL LIPASE [PUTATIVE] | Lipase |
| 10353 | 1334 | PHOSPHATIDATE CYTIDYLYLTRANSFERASE [PUTATIVE] | Transferases |
| 10360 | 1335 | PECTINESTERASE [PUTATIVE] | Esterase |
| 10368 | 1336 | 5-ENOLPYRUVYLSHIKIMATE-3-PHOSPHATE (EPSP) SYNTHASE IDENTICAL TO GB:X06613:ATEPSPS | Synthase |
| 10369 | 1337 | NUCLEOTIDE SUGAR EPIMERASE [PUTATIVE] | Epimerase |
| 10372 | 1338 | RECEPTOR-LIKE PROTEIN KINASE [PUTATIVE] | Kinase, Protein |
| 10377 | 1339 | FLAVONOL REDUCTASE [PUTATIVE] | Reductase |
| 10381 | 1340 | DIHYDRODIPICOLINATE SYNTHASE [PUTATIVE] | Synthase |
| 10396 | 1341 | PROTEIN KINASE CONTAINS A PROTEIN KINASE DOMAIN PROFILE (PDOC00100)[PUTATIVE] | Kinase, Protein |
| 10425 | 1342 | BETA-AMYLASE [PUTATIVE] | Glycosylase |
| 10448 | 1343 | 3-METHYL-2-OXOBUTANOATE HYDROXY-METHYL- TRANSFERASE | Transferases |
| 10479 | 1344 | CYCLIC NUCLEOTIDE-REGULATED ION CHANNEL PROTEIN [PUTATIVE] | Channel |
| 10480 | 1345 | CYCLIC NUCLEOTIDE-REGULATED ION CHANNEL PROTEIN [PUTATIVE] | Channel |
| 10481 | 1346 | CYCLIC NUCLEOTIDE-REGULATED ION CHANNEL PROTEIN [PUTATIVE] | Channel |
| 10508 | 1347 | BETA-KETOACYL-COA SYNTHASE [PUTATIVE] | Synthase |
| 10521 | 1348 | SER/THR PROTEIN KINASE [PUTATIVE] | Kinase, Protein |
| 10522 | 1349 | INORGANIC PYROPHOSPHATASE PARTIAL[PUTATIVE] | 3' Phosphatase |
| 10529 | 1350 | PECTINESTERASE [PUTATIVE] | Esterase |
| 10539 | 1351 | PECTINESTERASE [PUTATIVE] | Esterase |
| 10540 | 1352 | PECTINESTERASE [PUTATIVE] | Esterase |
| 10541 | 1353 | PECTINESTERASE [PUTATIVE] | Esterase |
| 10547 | 1354 | ALCOHOL DEHYDROGENASE [PUTATIVE] | Dehydrogenases |
| 10548 | 1355 | ALCOHOL DEHYDROGENASE [PUTATIVE] | Dehydrogenases |

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| 10549 | 1356 | ALCOHOL DEHYDROGENASE [PUTATIVE] | Dehydrogenases |
| 10550 | 1357 | ALCOHOL DEHYDROGENASE [PUTATIVE] | Dehydrogenases |
| 10553 | 1358 | GALACTINOL SYNTHASE [PUTATIVE] | Synthase |
| 10563 | 1359 | PECTINESTERASE [PUTATIVE] | Esterase |
| 10567 | 1360 | PEPTIDYL-PROLYL CIS-TRANS ISOMERASE [PUTATIVE] | Isomerase |
| 10578 | 1361 | HISTIDINE KINASE IDENTICAL TO GB:D87545[PUTATIVE] | Kinase, Protein |
| 10590 | 1362 | PECTINESTERASE [PUTATIVE] | Esterase |
| 10594 | 1363 | PHOTOLYASE/BLUE-LIGHT RECEPTOR (PHR2) | Receptor |
| 10598 | 1364 | PHOSPHOLIPASE [PUTATIVE] | Lipase |
| 10602 | 1365 | PECTINESTERASE [PUTATIVE] | Esterase |
| 10608 | 1366 | GLUTATHIONE S-TRANSFERASE (GST6) IDENTICAL TO GB:X95295. BASED ON IDENTICAL CDNA HITS, THE TRANSLATION IS NOW 40 AAS LONGER AT THE N-TERMINAL, AND START OF EXON2 IS ALSO CORRECTED. | Transferases |
| 10628 | 1367 | SERINE PROTEASE [PUTATIVE] | Protease |
| 10636 | 1368 | PROTEIN KINASE CONTAINS A PROTEIN KINASE DOMAIN PROFILE (PDOC00100)[PUTATIVE] | Kinase, Protein |
| 10644 | 1369 | PROTEIN KINASE | Kinase, Protein |
| 10645 | 1370 | EXONUCLEASE CONTAINS ZINC-FINGER C2H2-TYPE DOMAIN; SIMILAR TO X.LAEVIS XPMC2 PROTEIN (XPMC2 PREVENTS MITOTIC CATASTROPHE IN FISSION YEAST)[PUTATIVE] | Nuclease |
| 10670 | 1371 | GLYCOGEN SYNTHASE SIMILAR TO GLYCOGEN SYNTHASE PRECURSOR (GRANULE-BOUND STARCH SYNTHASE II) GB:Q43093 FROM [PISUM SATIVUM][PUTATIVE] | Synthase |
| 10671 | 1372 | PEROXIDASE VERY SIMILAR TO PEROXIDASE GB:CAA66963 FROM [ARABIDOPSIS THALIANA][PUTATIVE] | Oxidase |
| 10678 | 1373 | ALDOSE 1-EPIMERASE SHOWS SIMILARITY TO ALDOSE EPIMERASES[PUTATIVE] | Epimerase |

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| 10679 | 1374 | PECTATE LYASE SIMILAR TO PECTATE LYASE PRECURSOR GB:P40973 [LILIUM LONGIFLORUM][PUTATIVE] | Lyase |
| 10680 | 1375 | VOLTAGE-DEPENDENT ANION-SELECTIVE CHANNEL PORIN SIMILAR TO OUTER MITOCHONDRIAL MEMBRANE PORIN (VOLTAGE-DEPENDENT ANION- SELECTIVE CHANNEL PROTEIN) (VDAC) (POM 34) GB:P42055 [SOLANUM TUBEROSUM][PUTATIVE] | Channel |
| 10682 | 1376 | PROTEIN KINASE SIMILAR TO PROTEIN KINASE APK1A GB:Q06548 [ARABIDOPSIS THALIANA][PUTATIVE] | Kinase, Protein |
| 10691 | 1377 | VACUOLAR MEMBRANE ATPASE SUBUNIT G (AVMA10) IDENTICAL TO VACUOLAR MEMBRANE ATPASE SUBUNIT G (AVMA10) GB:AF181688 [ARABIDOPSIS THALIANA] | ATPase |
| 10702 | 1378 | CARBONIC ANHYDRASE, CHLOROPLAST PRECURSOR IDENTICAL TO CARBONIC ANHYDRASE, CHLOROPLAST PRECURSOR GB:P27140 [ARABIDOPSIS THALIANA] | Anhydrase |
| 10714 | 1379 | BETA-1,4-N-ACETYLGLUCOSAMINYLTRANSFERASE GB:AAD31053 [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN SIMILAR TO][PUTATIVE] | Transferases |
| 10728 | 1380 | AMINO ACID PERMEASE SIMILAR TO AMINO ACID PERMEASE GB:AAB71468 [ARABIDOPSIS THALIANA][PUTATIVE] | Transporter |
| 10734 | 1381 | ADENYLATE KINASE SIMILAR TO ADK ADENYLATE KINASE GB:S50007 [STREPTOMYCES COELICOLOR][PUTATIVE] | Kinase |
| 10736 | 1382 | PROTEIN KINASE C-TERMINAL REGION SIMILAR TO PROTEIN KINASES: GB:S71277 [ARABIDOPSIS THALIANA], GB:CAB43834 [ARABIDOPSIS THALIANA]; PFAM HMM HIT: EUKARYOTIC PROTEIN KINASE DOMAIN[PUTATIVE] | Kinase, Protein |
| 10750 | 1383 | DEHYDROGENASE CONTAINS PFAM PROFILES: PF00106 SHORT CHAIN DEHYDROGENASE, PF00678 SHORT CHAIN DEHYDROGENASE/REDUCTASE C- TERMINUS[PUTATIVE] | Dehydrogenases |

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| 10751 | 1384 | URIDYLYL TRANSFERASE-LIKE PROTEINS GB:AAD20075, GB:AAC00631 [ARABIDOPSIS THALIANA]; UNKNOWN PROTEIN SIMILAR TO | Transferases |
| 10754 | 1385 | ASPARTATE KINASE SIMILAR TO ASPARTATE KINASE GB:CAA67376 [ARABIDOPSIS THALIANA][PUTATIVE] | Kinase |
| 10757 | 1386 | POTASSIUM TRANSPORTER SIMILAR TO POTASSIUM TRANSPORTER GB:AAB87687 [ARABIDOPSIS THALIANA][PUTATIVE] | Transporter |
| 10762 | 1387 | UDP-GLUCOSYL TRANSFERASE SIMILAR TO UDP- GLUCOSE GLUCOSYLTRANSFERASE GB:BAA34687, INDOLE-3-ACETATE BETA-GLUCOSYLTRANSFERASE GB:Q41819 [ZEA MAYS]; CONTAINS PFAM PROFILE: UDP-GLUCORONOSYL AND UDP-GLUCOSYL TRANSFERASES[PUTATIVE] | Transferases |
| 10765 | 1388 | PROTEIN KINASE CONTAINS PFAM PROFILE: EUKARYOTIC PROTEIN KINASE DOMAIN[PUTATIVE] | Kinase, Protein |
| 10772 | 1389 | PHYTOCHELATIN SYNTHETASE GB:CAA07251 [ARABIDOPSIS THALIANA], PFAM HMM HIT: TNFR/NGFR CYSTEINE-RICH REGION, UNKNOWN PROTEIN SIMILAR TO PUTATIVE | Synthase |
| 10792 | 1390 | COESTERASE DOMAIN | Esterase |
| 10812 | 1391 | STEAROYL-ACYL CARRIER PROTEIN DESATURASE SIMILAR TO STEAROYL-ACYL CARRIER PROTEIN DESATURASE GB:CAA07349 FROM [LINUM USITATISSIMUM][PUTATIVE] | Desaturases |
| 10813 | 1392 | STEAROYL-ACYL CARRIER PROTEIN DESATURASE SIMILAR TO STEAROYL-ACYL CARRIER PROTEIN DESATURASE GB:CAA07349 FROM [LINUM USITATISSIMUM][PUTATIVE] | Desaturases |
| 10814 | 1393 | STEAROYL-ACYL CARRIER PROTEIN DESATURASE SIMILAR TO STEAROYL-ACYL CARRIER PROTEIN DESATURASE GB:CAA07349 FROM [LINUM USITATISSIMUM][PUTATIVE] | Desaturases |
| 10825 | 1394 | ASPARTYL PROTEASE CONTAINS PFAM PROFILE: PF00026 EUKARYOTIC ASPARTYL PROTEASE[PUTATIVE] | Protease |

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| 10826 | 1395 | PROTEIN PHOSPHATASE-2C (PP2C) SIMILAR TO PUTATIVE PROTEIN PHOSPHATASE-2C (PP2C) GB:AAC36699 [MESEMBRYANTHEMUM CRYSTALLINUM][PUTATIVE] | Phosphatase |
| 10828 | 1396 | S-ADENOSYLMETHIONINE:2-DEMETHYLMENAQUINONE METHYLTRANSFERASE SIMILAR TO S-ADENOSYLMETHIONINE:2-DEMETHYLMENAQUINONE METHYLTRANSFERASE GB:P32165 [ESCHERICHIA COLI][PUTATIVE] | Transferases |
| 10832 | 1397 | PROTEIN KINASE CONTAINS PFAM PROFILE: PF00069 EUKARYOTIC PROTEIN KINASE DOMAIN[PUTATIVE] | Kinase, Protein |
| 10839 | 1398 | IAA-AMINO ACID HYDROLASE (ILR1) IDENTICAL TO IAA-AMINO ACID HYDROLASE (ILR1) GB:U23794 [ARABIDOPSIS THALIANA] | Hydrolase |
| 10840 | 1399 | PROTEIN KINASE CONTAINS PFAM PROFILES: PF00069 EUKARYOTIC PROTEIN KINASE DOMAIN, PF00560 LEUCINE RICH REPEAT (5 COPIES)[PUTATIVE] | Kinase, Protein |
| 10850 | 1400 | N-ACETLYLTRANSFERASE CONTAINS PFAM PROFILE: PF00583 ACETYLTRANSFERASE (GNAT) FAMILY[PUTATIVE] | Transferases |
| 10857 | 1401 | CELLULOSE SYNTHASE CATALYTIC SUBUNIT SIMILAR TO CELLULOSE SYNTHASE CATALYTIC SUBUNIT GB:AAD40885 FROM [ARABIDOPSIS THALIANA][PUTATIVE] | Synthase |
| 10871 | 1402 | GLUTATHIONE S-TRANSFERASE IDENTICAL TO GLUTATHIONE S-TRANSFERASE GB:AAB09584 FROM [ARABIDOPSIS THALIANA] | Transferases |
| 10906 | 1403 | PHOSPHOLIPASE SIMILAR TO UNKNOWN PROTEIN GB:AAC32238 [ARABIDOPSIS THALIANA], POTENTIAL PHOSPHOLIPASE C- SIMILAR TO MULTIPLE PHOSPHOLIPASE PROTEINS FROM MYCOBACTERIUM SPECIES: GB:CAB06146, GB:CAB06147, GB:AAC18944, GB:CAB44656[PUTATIVE] | Lipase |
| 10919 | 1404 | PEROXIDASE SIMILAR TO PEROXIDASE GB:CAA66966 [ARABIDOPSIS THALIANA][PUTATIVE] | Oxidase |

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| 10920 | 1405 | PHOSPHORIBOSYLANTHRANILATE TRANSFERASE SIMILAR TO PHOSPHORIBOSYLANTHRANILATE TRANSFERASE GB:CAA16616 [ARABIDOPSIS THALIANA], PHOSPHORIBOSYLANTHRANILATE TRANSFERASE GB:BAA13032 [PISUM SATIVUM][PUTATIVE] | Transferases |
| 10929 | 1406 | SER/THR PROTEIN KINASE DOMAIN, SIMILAR TO SERINE/THREONINE PROTEIN KINASE PTO GB:AAB47421 [LYCOPERSICON ESCULENTUM] | Kinase, Protein |
| 10930 | 1407 | METHIONINE SYNTHASE SIMILAR TO COBALAMIN- INDEPENDENT METHIONINE SYNTHASE GB:AAC50037 [ARABIDOPSIS THALIANA][PUTATIVE] | Synthase |
| 10950 | 1408 | SHORT-CHAIN TYPE DEHYDROGENASE/REDUCTASE SIMILAR TO SHORT-CHAIN TYPE DEHYDROGENASE/REDUCTASE GB:Q08632 [PICEA ABIES][PUTATIVE] | Dehydrogenase |
| 10952 | 1409 | SHORT-CHAIN TYPE DEHYDROGENASE/REDUCTASE SIMILAR TO SHORT-CHAIN TYPE DEHYDROGENASE/REDUCTASE GB:Q08632 [PICEA ABIES][PUTATIVE] | Dehydrogenase |
| 10953 | 1410 | BETA-1,3-GLUCANASE SIMILAR TO BETA-1,3- GLUCANASE GB:S12402 [NICOTIANA SP], GB:CAA03908 [CITRUS SINENSIS], GB:S44364 [LYCOPERSICON ESCULENTUM][PUTATIVE] | Glycosylase |
| 10963 | 1411 | GLUTAMATE RECEPTOR (GLR1) IDENTICAL TO PUTATIVE GLUTAMATE RECEPTOR (GLR1) GB:AF079998 [ARABIDOPSIS THALIANA][PUTATIVE] | Receptor |
| 10981 | 1412 | LIPASE/HYDROLASE GDSL-LIKE MOTIF; PUTATIVE CONTAINS PFAM PROFILE: PF00657 LIPASE/ACYLHYDROLASE | Lipase |
| 11010 | 1413 | ETHYLENE RECEPTOR (EIN4) SIMILAR TO ETHYLENE RECEPTOR GB:AAC31123 [MALUS DOMESTICA], IDENTICAL TO PUTATIVE ETHYLENE RECEPTOR GB:AAD02485 [ARABIDOPSIS THALIANA]; PFAM HMM HIT: RESPONSE REGULATOR RECEIVER DOMAIN, SIGNAL C TERMINAL DOMAIN[PUTATIVE] | Receptor |

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| 11022 | 1414 | PROTEIN KINASE SIMILAR TO HYPOTHETICAL PROTEIN WHICH CONTAINS EUKARYOTIC PROTEIN KINASE DOMAIN PF00069 GB:CAB51834 [ORYZA SATIVA]; PFAM HMM HIT: EUKARYOTIC PROTEIN KINASE DOMAIN[PUTATIVE] | Kinase, Protein |
| 11032 | 1415 | RIBOSE 5-PHOSPHATE ISOMERASE IDENTICAL TO PUTATIVE RIBOSE 5-PHOSPHATE ISOMERASE GB:AAD57010 [ARABIDOPSIS THALIANA]; SIMILAR TO RIBOSE 5-PHOSPHATE ISOMERASES: GB:BAA10413 [SYNECHOCYSTIS SP], GB:CAB49687 [PYROCOCCUS ABYSSI], GB:S22097 [ESCHERICHIA COLI][PUTATIVE] | Isomerase |
| 11040 | 1416 | ZETA-CAROTENE DESATURASE PRECURSOR NEARLY IDENTICAL TO ZETA-CAROTENE DESATURASE PRECURSOR GB:AAA91161 [ARABIDOPSIS THALIANA][PUTATIVE] | Desaturases |
| 11067 | 1417 | SERINE/THREONINE PROTEIN KINASE SIMILAR TO MANY OTHER PUTATIVE PROTEIN KINASES[PUTATIVE] | Kinase, Protein |
| 11072 | 1418 | BRANCHED-CHAIN AMINO ACID AMINOTRANSFERASE [PUTATIVE] | Transferases |
| 11076 | 1419 | SIGNAL PEPTIDASE MICROSOMAL GB:P28687 FROM [GALLUS GALLUS] | Protease |
| 11079 | 1420 | GLUCOSE AND RIBITOL DEHYDROGENASE HOMOLOG SIMILAR TO GB:AAC60580 FROM [HORDEUM VULGARE] SHOWING HOMOLOGIES TO BACTERIAL GLUCOSE AND RIBITOL DEHYDROGENASES[PUTATIVE] | Dehydrogenases |
| 11114 | 1421 | PECTINESTERASE SIMILAR TO PECTINESTERASE PRECURSOR GB:Q42920 FROM [MEDICAGO SATIVA][PUTATIVE] | Esterase |
| 11115 | 1422 | PECTINESTERASE SIMILAR TO PECTINESTERASE PPE8B PRECURSOR GB:Q43062 FROM [PRUNUS PERSICA][PUTATIVE] | Esterase |
| 11117 | 1423 | PROTEIN PHOSPHATASE-2C SIMILAR TO PROTEIN PHOSPHATASE-2C GB:AAC36699 FROM [MESEMBRYANTHEMUM CRYSTALLINUM][PUTATIVE] | Phosphatase |

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| 11144 | 1424 | PECTINACETYLESTERASE SIMILAR TO GB:CAA67728 FROM [VIGNA RADIATA][PUTATIVE] | Esterase |
| 11152 | 1425 | RECEPTOR PROTEIN KINASES: GB:CAB43834, GB:S71277 [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN SIMILAR TO] | Kinase, Protein |
| 11158 | 1426 | ALKYL HYDROPEROXIDE REDUCTASE AND THIOL-SPECIFIC ANTIOXIDANT FAMILY | Reductase |
| 11164 | 1427 | DUAL-SPECIFICITY PROTEIN PHOSPHATASE SIMILAR TO DUAL-SPECIFICITY PROTEIN PHOSPHATASE GB:CAA77232 [ARABIDOPSIS THALIANA][PUTATIVE] | Phosphatase |
| 11173 | 1428 | GUANYLATE KINASE SIMILAR TO GUANYLATE KINASE (GMK) GB:AAD31506 [SALMONELLA TYPHIMURIUM]; CONTAINS PFAM PROFILE: PF00625 GUANYLATE KINASE[PUTATIVE] | Kinase |
| 11179 | 1429 | GLYCOSYL TRANSFERASE CONTAINS PFAM PROFILE: PF01501 GLYCOSYL TRANSFERASE FAMILY 8[PUTATIVE] | Transferases |
| 11180 | 1430 | PROTEIN PHOSPHATASE-2C (PP2C) SIMILAR TO PROTEIN PHOSPHATASE-2C (PP2C) GB:AAC36699 [MESEMBRYANTHEMUM CRYSTALLINUM]; CONTAINS PFAM PROFILE: PF00481 PROTEIN PHOSPHATASE 2C[PUTATIVE] | Phosphatase |
| 11183 | 1431 | PROLYL 4-HYDROXYLASE ALPHA SUBUNIT PRECURSOR GB:P54001 [RATTUS NORVEGICUS] [UNKNOWN PROTEIN SIMILAR TO C-TERMINAL PORTION OF] | Hydroxylase |
| 11188 | 1432 | DEHYDROQUINASE SHIKIMATE DEHYDROGENASE SIMILAR TO DEHYDROQUINASE SHIKIMATE DEHYDROGENASE GB:S46210 [NICOTIANA TABACUM][PUTATIVE] | Dehydrogenases |
| 11203 | 1433 | PYRUVATE DEHYDROGENASE KINASE, 3' PARTIAL SIMILAR TO PYRUVATE DEHYDROGENASE KINASE GB:AAC97601 FROM [ARABIDOPSIS THALIANA][PUTATIVE] | Dehydrogenase |
| 11206 | 1434 | BETA-GLUCOSIDASE, PUTATIVE SIMILAR TO BETA-GLUCOSIDASE GB:AAF23823 FROM [ARABIDOPSIS THALIANA] | Glycosylase |

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| 11236 | 1435 | POLYGALACTURONASE, UNKNOWN PROTEIN CONTAINS PFAM PROFILE:PF00295 | Glycosylase |
| 11242 | 1436 | PECTIN METHYLESTERASE, PUTATIVE SIMILAR TO PECTIN METHYLESTERASE GB:BAA89480 FROM [SALIX GILGIANA] | Esterase |
| 11251 | 1437 | ASPARTATE PHOSPHATASE, HYPOTHETICAL PROTEIN CONTAINS PFAM PROFILE: PF00987 RAPA-LIKE BACTERIAL PROTEIN ASPARTATE PHOSPHATASE | Phosphatase |
| 11254 | 1438 | TRNA PSEUDOURIDINE SYNTHASE SIMILAR TO TRNA PSEUDOURIDINE SYNTHASE A GB:P07649 [ESCHERICHIA COLI][PUTATIVE] | Synthase |
| 11260 | 1439 | PECTATE LYASE SIMILAR TO PECTATE LYASE 2 GB:AAF19196 [MUSA ACUMINATA][PUTATIVE] | Lyase |
| 11261 | 1440 | UDP-GLUCOSE:STEROL GLUCOSYLTRANSFERASE UDP-GLUCOSE:STEROL GLUCOSYLTRANSFERASE GB:Z83833 [ARABIDOPSIS THALIANA] | Transferases |
| 11266 | 1441 | PROTEIN KINASE SIMILAR TO APK1A PROTEIN KINASE GB:Q06548 [ARABIDOPSIS THALIANA]; CONTAINS PFAM PROFILE: PF00069 EUKARYOTIC PROTEIN KINASE DOMAIN[PUTATIVE] | Kinase, Protein |
| 11272 | 1442 | PURPLE ACID PHOSPHATASE SIMILAR TO PURPLE ACID PHOSPHATASE GB:CAA06921 [IPOMOEA BATATAS][PUTATIVE] | Phosphatase |
| 11275 | 1443 | GLUCAN SYNTHASE SIMILAR TO GLUCAN SYNTHASE GB:AAD11794 [FILOBASIDIELLA NEOFORMANS VAR. NEOFORMANS][PUTATIVE] | Synthase |
| 11286 | 1444 | GTP CYCLOHYDROLASE I SIMILAR TO GTP CYCLOHYDROLASE I GB:P22288 [RATTUS NORVEGICUS]; CONTAINS PFAM PROFILE: PF01227 GTP CYCLOHYDROLASE I | Hydrolase |
| 11291 | 1445 | BETA-1,3-GLUCANASE PRECURSOR SIMILAR TO BETA- 1,3-GLUCANASE PRECURSOR GB:AAD10386 [ORYZA SATIVA]; CONTAINS PFAM PROFILE: PF00332 GLYCOSYL HYDROLASES FAMILY 17[PUTATIVE] | Hydrolase |
| 11292 | 1446 | GLUCOSYLTRANSFERASE GB:AAD23884 [ARABIDOPSIS THALIANA], UNKNOWN PROTEIN SIMILAR TO PUTATIVE | Transferases |

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| 11311 | 1447 | GLUTAMATE RECEPTOR GB:AAD09173 [ARABIDOPSIS THALIANA] AND PUTATIVE LIGAND-GATED IONIC CHANNEL GB:AAC33237 [ARABIDOPSIS THALIANA], PUTATIVE | Channel |
| 11323 | 1448 | PREPHENATE DEHYDRATASE, P-PROTEIN: CHORISMATE MUTASE, SIMILAR TO P-PROTEIN: CHORISMATE MUTASE, PREPHENATE DEHYDRATASE GB:P43900 [HAEMOPHILUS INFLUENZAE][PUTATIVE] | Dehydratase |
| 11327 | 1449 | RIBULOSE-1,5-BISPHOSPHATE CARBOXYLASE/OXYGENASE SMALL SUBUNIT N-METHYLTRANSFERASE I SIMILAR TO RIBULOSE-1,5-BISPHOSPHATE CARBOXYLASE/OXYGENASE SMALL SUBUNIT N-METHYLTRANSFERASE I GB:AAC29137 [CHLOROPLAST SPINACIA OLERACEA][PUTATIVE] | Transferases |
| 11342 | 1450 | POLYGALACTURONASE (PGA3) IDENTICAL TO POLYGALACTURONASE (PGA3) GB:AJ005584 (MOL. GEN. GENET. 261 (6), 948-952 (1999)) | Glycosylase |
| 11343 | 1451 | POLYGALACTURONASE SIMILAR TO POLYGALACTURONASE GB:CAA05892 [ARABIDOPSIS THALIANA][PUTATIVE] | Glycosylase |
| 11344 | 1452 | POLYGALACTURONASE SIMILAR TO POLYGALACTURONASE GB:CAA05892 [ARABIDOPSIS THALIANA][PUTATIVE] | Glycosylase |
| 11345 | 1453 | EXOPOLYGALACTURONASE IDENTICAL TO EXOPOLYGALACTURONASE GB:X72292 (MOL. GEN. GENET. 261 (6), 948-952 (1999)) | Glycosylase |
| 11357 | 1454 | POLYGALACTURONASE SIMILAR TO POLYGALACTURONASE GB:AAC26512 [CUCUMIS MELO]; CONTAINS NON-CONSENSUS AA DONOR SPLICE SITE AT EXON 2[PUTATIVE] | Glycosylase |
| 11383 | 1455 | PROTEIN KINASE CONTAINS PFAM PROFILE: PF00069 EUKARYOTIC PROTEIN KINASE DOMAIN, PF00560 LEUCINE RICH REPEAT (5 COPIES)[PUTATIVE] | Kinase, Protein |
| 11391 | 1456 | PROTEIN KINASE CONTAINS PFAM PROFILE: PF00069 EUKARYOTIC PROTEIN KINASE DOMAIN (2 COPIES)[PUTATIVE] | Kinase, Protein |

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| 11398 | 1457 | D-ALANINE:D-LACTATE LIGASE GB:AAD41882 [ENTEROCOCCUS FAECIUM][HYPOTHETICAL PROTEIN SIMILAR TO] | Ligase |
| 11402 | 1458 | SERINE/THREONINE PROTEIN KINASE SIMILAR TO SERINE/THREONINE-SPECIFIC KINASE GB:S68589 [ARABIDOPSIS THALIANA]; PFAM HMM HITS: PUTATIVE SERINE/THREONINE PROTEIN KINASE, EUKARYOTIC PROTEIN KINASE DOMAIN[PUTATIVE] | Kinase, Protein |
| 11405 | 1459 | BETA-GLUCAN SYNTHASE - REVERSIBLY GLYCOSYLATABLE POLYPEPTIDE SIMILAR TO REVERSIBLY GLYCOSYLATABLE POLYPEPTIDE GB:AAB88408 [PISUM SATIVUM] (POSSIBLE COMPONENT OF GOLGI [PUTATIVE] | Synthase |
| 11413 | 1460 | MITOCHONDRIAL INNER MEMBRANE PROTEASE SUBUNIT 2 SIMILAR TO MITOCHONDRIAL INNER MEMBRANE PROTEASE SUBUNIT 2 GB:P46972 [SACCHAROMYCES CEREVISIAE], IDENTICAL TO PUTATIVE SIGNAL PEPTIDASE GB:AAD56314 [ARABIDOPSIS THALIANA]; PFAM HMM HIT: SIGNAL PEPTIDASES I[PUTATIVE] | Protease |
| 11416 | 1461 | PROTEIN KINASE PFAM HMM HIT: EUKARYOTIC PROTEIN KINASE DOMAIN; SIMILAR TO PUTATIVE RECEPTOR SER/THR PROTEIN KINASE GB:AAD56317 [ARABIDOPSIS THALIANA][PUTATIVE] | Kinase, Protein |
| 11438 | 1462 | PROTEIN KINASE SIMILAR TO HYPOTHETICAL PROTEINS GB:AAC13615, GB:CAA18746, GB:AAB81672 [ARABIDOPSIS THALIANA]; CONTAINS PFAM PROFILE: EUKARYOTIC PROTEIN KINASE DOMAIN[PUTATIVE] | Kinase, Protein |
| 11441 | 1463 | GLUTATHIONE TRANSFERASE SIMILAR TO GLUTATHIONE TRANSFERASE GB:CAA71784 [GLYCINE MAX][PUTATIVE] | Transferases |
| 11455 | 1464 | PECTINACETYLESTERASE SIMILAR TO PECTINACETYLESTERASE PRECURSOR GB:CAA67728 [VIGNA RADIATA][PUTATIVE] | Esterase |
| 11456 | 1465 | PECTINACETYLESTERASE SIMILAR TO PECTINACETYLESTERASE PRECURSOR GB:CAA67728 [VIGNA RADIATA][PUTATIVE] | Esterase |

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| 11465 | 1466 | NON-LTR REVERSE TRANSCRIPTASE SIMILAR TO PUTATIVE NON-LTR REVERSE TRANSCRIPTASE INCLUDING GB:AAD20714 AND GB:AAD24831[PUTATIVE] | Transcriptase |
| 11472 | 1467 | PHYTOENE DESATURASE GB:P28553 FROM [GLYCINE MAX][PUTATIVE, OXIDOREDUCTASE SIMILAR TO] | Desaturases |
| 11478 | 1468 | ASCORBATE PEROXIDASE STRONG SIMILARITY TO ASCORBATE PEROXIDASE GB:CAA56340[PUTATIVE] | Oxidase |
| 11497 | 1469 | PROTEIN KINASE SIMILAR TO PROTEIN KINASE (APK1A) GB:Q06548 [ARABIDOPSIS THALIANA]; CONTAINS PFAM PROFILE: PF00069 EUKARYOTIC PROTEIN KINASE DOMAIN[PUTATIVE] | Kinase, Protein |
| 11507 | 1470 | LIPASE/HYDROLASE GDSE-LIKE MOTIF; PUTATIVE CONTAINS PFAM PROFILE: PF00657 LIPASE/ACYLHYDROLASE | Lipase |
| 11515 | 1471 | ENDONUCLEASE III HOMOLOGS: GB:AAD35453, GB:BAA79061, GB:CAB49586[HYPOTHETICAL PROTEIN SIMILAR TO] | Nuclease |
| 11517 | 1472 | URIDYLATE KINASE SIMILAR TO URIDYLATE KINASE GB:CAB13524 [BACILLUS SUBTILIS], GB:P74457 [SYNECHOCYSTIS PCC6803][PUTATIVE] | Kinase |
| 11520 | 1473 | PEPTIDYL-PROLYL CIS-TRANS ISOMERASE FKBP-TYPE, UNKNOWN PROTEIN PFAM HMM HIT: | Isomerase |
| 11537 | 1474 | LYCOPENE BETA CYCLASE IDENTICAL TO LYCOPENE BETA CYCLASE GB:AAB53337 [ARABIDOPSIS THALIANA] | Cyclase |
| 11542 | 1475 | FATTY ACID ELONGASE 3-KETOACYL-COA SYNTHASE 1 SIMILAR TO FATTY ACID ELONGASE 3-KETOACYL-COA SYNTHASE 1 GB:AAC99312 [ARABIDOPSIS THALIANA][PUTATIVE] | Synthase |
| 11576 | 1476 | DIADENOSINE 5',5"-P ₁ ,P ₄ -TETRAPHOSPHATE HYDROLASE SIMILAR TO DIADENOSINE 5',5"-P ₁ ,P ₄ -TETRAPHOSPHATE HYDROLASE GB:AAC49902 [LUPINUS ANGUSTIFOLIUS], PFAM HMM HIT: BACTERIAL MUTT PROTEIN[PUTATIVE] | Hydrolase |

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| 11577 | 1477 | MANNOSYLTRANSFERASE [ESCHERICHIA COLI], UNKNOWN PROTEIN C- TERMINAL PORTION SIMILAR TO | GB:BAA28328 | Transferases |
| 11581 | 1478 | ABC TRANSPORTER ATPASE SIMILAR TO ABC TRANSPORTER ATPASE GB:AAC68280 [CHLAMYDIA TRACHOMATIS][PUTATIVE] | | Transporter |
| 11584 | 1479 | GALACTOKINASE, 5' PARTIAL SIMILAR TO GALACTOKINASE GB:BAA84705 [MUS MUSCULUS][PUTATIVE] | | Kinase |
| 11585 | 1480 | PECTINESTERASE CONTAINS SIMILARITY TO PECTINESTERASE GB:AAB57671 [CITRUS SINENSIS][PUTATIVE] | | Esterase |
| 11586 | 1481 | PECTINESTERASE CONTAINS SIMILARITY TO PECTINESTERASE GB:AAB57671 [CITRUS SINENSIS][PUTATIVE] | | Esterase |
| 11588 | 1482 | ALPHA-L-ARABINOFURANOSIDASE CONTAINS SIMILARITY TO ALPHA-L-ARABINOFURANOSIDASE A PRECURSOR GB:P42254 [ASPERGILLUS NIGER][PUTATIVE] | | Glycosylase |
| 11598 | 1483 | ALPHA/BETA HYDROLASE CONTAINS PFAM PROFILE: PF00561 ALPHA/BETA HYDROLASE FOLD; PREDICTED BY GENSCAN[PUTATIVE] | | Hydrolase |
| 11601 | 1484 | ALPHA-HYDROXYNITRILE LYASE SIMILAR TO ALPHA- HYDROXYNITRILE LYASE GB:CAA11219 [MANIHOT ESCULENTA][PUTATIVE] | | Lyase |
| 11603 | 1485 | (1-4)-BETA-MANNAN ENDOHYDROLASE SIMILAR TO (1-4)-BETA-MANNAN ENDOHYDROLASE GB:AAB87859 [LYCOPERSICON ESCULENTUM][PUTATIVE] | | Hydrolase |
| 11604 | 1486 | (1-4)-BETA-MANNAN ENDOHYDROLASE SIMILAR TO (1-4)-BETA-MANNAN ENDOHYDROLASE GB:AAB87859 [LYCOPERSICON ESCULENTUM][PUTATIVE] | | Hydrolase |
| 11631 | 1487 | LEUCOANTHOCYANIDIN DIOXYGENASE, PUTATIVE SIMILAR TO LEUCOANTHOCYANIDIN DIOXYGENASE SP:P51093 [VITIS VINIFERA (GRAPE)] | | Oxygenases |

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| 11645 | 1488 | GLUCOSYL TRANSFERASE, PUTATIVE SIMILAR TO ZEATIN O-XYLOSYLTRANSFERASE SP:P56725 [PHASEOLUS VULGARIS (KIDNEY BEAN) (FRENCH BEAN)] | Transferases |
| 11651 | 1489 | PROTEIN PHOSPHATASE 2C (PP2C) IDENTICAL TO PROTEIN PHOSPHATASE 2C (PP2C) GB:P49598 [ARABIDOPSIS THALIANA] | Phosphatase |
| 11676 | 1490 | DIGALACTOSYLDIACYLGLYCEROL SYNTHASE IDENTICAL TO DIGALACTOSYLDIACYLGLYCEROL SYNTHASE GB:AAD42378 [ARABIDOPSIS THALIANA] | Synthase |
| 11684 | 1491 | DIHYDRONEOPTERIN ALDOLASE SIMILAR TO DIHYDRONEOPTERIN ALDOLASE GB:P28823 [BACILLUS SUBTILIS][PUTATIVE] | Aldolase |
| 11714 | 1492 | DNA-3-METHLYADENINE GLYCOSYLASE (MAG) IDENTICAL TO DNA-3-METHLYADENINE GLYCOSYLASE (MAG) SP:Q39147 [ARABIDOPSIS THALIANA (MOUSE-EAR CRESS)] | Glycosylase |
| 11743 | 1493 | PEPTIDYL-PROLYL CIS-TRANS ISOMERASE FKBP-TYPE, PUTATIVE CONTAINS PFAM PROFILE:PF00254 FKBP-TYPE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE | Isomerase |
| 11759 | 1494 | CHITINASE BASIC, IDENTICAL TO BASIC CHITINASE GB:AAA32769 GI:166666 [ARABIDOPSIS THALIANA] (PLANT PHYSIOL. 93, 907-914 (1990)) | Chitinase |
| 11771 | 1495 | PROTEIN PHOSPHATASE 2C, PUTATIVE CONTAINS PFAM PROFILE: PF00481 PROTEIN PHOSPHATASE 2C | Phosphatase |
| 11784 | 1496 | ZINC TRANSPORTER IDENTICAL TO PUTATIVE ZINC TRANSPORTER GB:AAC24197 FROM [ARABIDOPSIS THALIANA], (PROC. NATL. ACAD. SCI. U.S.A. 95 (12), 7220-7224 (1998))[PUTATIVE] | Transporter |
| 11796 | 1497 | OXIDOREDUCTASES[HYPOTHETICAL PROTEIN SIMILAR TO] | Reductase |
| 11799 | 1498 | OXIDOREDUCTASES[HYPOTHETICAL PROTEIN SIMILAR TO] | Reductase |
| 11816 | 1499 | PROTEIN KINASE, 3' PARTIAL LEUCINE-RICH REPEAT TRANSMEMBRANE PROTEIN KINASE 1 GB:AAC27894 FROM [ZEA MAYS][PUTATIVE] | Kinase, Protein |

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| 11818 | 1500 | ABC TRANSPORTER, PUTATIVE SIMILAR TO ATMRP4 (TRANSPORT OF GLUTATHIONE-CONJUGATES INTO THE VACUOLE) GB:CAA05625 [ARABIDOPSIS THALIANA]; CONTAINS PFAM PROFILE: PF00005 ABC TRANSPORTER | Transporter |
| 11819 | 1501 | ABC TRANSPORTER, PUTATIVE SIMILAR TO ATMRP4 (TRANSPORT OF GLUTATHIONE-CONJUGATES INTO THE VACUOLE) GB:CAA05625 [ARABIDOPSIS THALIANA]; CONTAINS PFAM PROFILE: PF00005 ABC TRANSPORTER | Transporter |
| 11820 | 1502 | ABC TRANSPORTER, PUTATIVE SIMILAR TO ATMRP4 (TRANSPORT OF GLUTATHIONE-CONJUGATES INTO THE VACUOLE) GB:CAA05625 [ARABIDOPSIS THALIANA]; CONTAINS PFAM PROFILE: PF00005 ABC TRANSPORTER | Transporter |
| 11821 | 1503 | SERINE ACETYLTRANSFERASE (SAT-1) IDENTICAL TO SERINE ACETYLTRANSFERASE (SAT-1) GB:U22964 [ARABIDOPSIS THALIANA] (PLANT MOL. BIOL. 30 (5), 1041-1049 (1996)) | Transferases |
| 11843 | 1504 | LOW AFFINITY CALCIUM ANTIporter CAX2 ALMOST IDENTICAL TO GB:AAB05914 FROM [ARABIDOPSIS THALIANA], CONTAINS PFAM PROFILE: PF00002 7 TRANSMEMBRANE RECEPTOR (SECRETIN FAMILY), AND PF01699 SODIUM/CALCIUM EXCHANGER PROTEIN | Transporter |
| 11849 | 1505 | BRASSINOSTEROID RECEPTOR KINASE, PUTATIVE SIMILAR TO GB:AAC49810 FROM [ARABIDOPSIS THALIANA], CONTAINS PFAM PROFILES: PF00560 LEUCINE RICH REPEAT (23 COPIES) | Kinase, Protein |
| 11850 | 1506 | L-ASCORBATE OXIDASE PRECURSOR, PUTATIVE SIMILAR TO GB:Q00624 FROM [BRASSICA NAPUS] (PLANT J. 2 (3), 331-342 (1992)) | Oxidase |
| 11851 | 1507 | POLLEN SPECIFIC PROTEIN, PUTATIVE SIMILAR TO GB:CAB59910 FROM [ARABIDOPSIS THALIANA], CONTAINS PFAM PROFILES: PF00394 MULTICOPPER OXIDASE | Oxidase |

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| 11868 | 1508 | GLUCAN ENDO-1,3-BETA-GLUCOSIDASE PRECURSOR, PUTATIVE SIMILAR TO GB:P52409 FROM [TRITICUM AESTIVUM] | Glycosylase |
| 11874 | 1509 | TRANSPORTER PROTEINS[HYPOTHETICAL PROTEIN CONTAINS SIMILARITY TO] | Transporter |
| 11887 | 1510 | PROTEIN KINASE, PUTATIVE SIMILAR TO PROTEIN KINASE GB:BAA24694 FROM [ARABIDOPSIS THALIANA] | Kinase, Protein |
| 11899 | 1511 | BETA-FRUCTOFURANOSIDASE, PUTATIVE SIMILAR TO BETA-FRUCTOFURANOSIDASE 1 GB:S37212 FROM [ARABIDOPSIS THALIANA] | Glycosylase |
| 11900 | 1512 | BETA-FRUCTOFURANOSIDASE 1 IDENTICAL TO GB:S37212 FROM [ARABIDOPSIS THALIANA] | Glycosylase |
| 11901 | 1513 | HYDROLASE, PUTATIVE SIMILAR TO METAL DEPENDENT HYDROLASE GB:AAD18619 FROM [CHLAMYDOPHILA PNEUMONIAE] | Hydrolase |
| 11925 | 1514 | POLYGALACTURONASE SIMILAR TO POLYGALACTURONASE GB:CAA11160 FROM [ARABIDOPSIS THALIANA][PUTATIVE] | Glycosylase |
| 11926 | 1515 | GTP PYROPHOSPHOKINASE SIMILAR TO GTP PYROPHOSPHOKINASE GB:O87331 FROM [CORYNEBACTERIUM GLUTAMICUM][PUTATIVE] | Kinase |
| 11928 | 1516 | PROTEASE, 5'PARTIAL SIMILAR TO SERINE PROTEASE GB:CAA07250 FROM [LYCOPERSICON ESCULENTUM][PUTATIVE] | Protease |
| 11944 | 1517 | LIPASE/HYDROLASE GDSL-LIKE MOTIF; MYROSINASE-ASSOCIATED PROTEIN, PUTATIVE SIMILAR TO GB:CAA71238 FROM [BRASSICA NAPUS], CONATAINS PFAM PROFILE:PF00657 | Lipase |
| 11954 | 1518 | PECTIN METHYLESTERASE SIMILAR TO PECTINESTERASE GB:Q43867 FROM [ARABIDOPSIS THALIANA][PUTATIVE] | Esterase |
| 11955 | 1519 | PECTIN METHYLESTERASE SIMILAR TO PECTIN METHYLESTERASE GB:Q42534 FROM [ARABIDOPSIS THALIANA][PUTATIVE] | Esterase |

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| 11959 | 1520 | LEUCINE-RICH REPEAT TRANSMEMBRANE PROTEIN KINASE SIMILAR TO LEUCINE-RICH REPEAT TRANSMEMBRANE PROTEIN KINASE 1 GB:AAC27894 FROM [ZEA MAYS][PUTATIVE] | Kinase, Protein |
| 11963 | 1521 | DIAMINOPIMELATE DECARBOXYLASE SIMILAR TO DIAMINOPIMELATE DECARBOXYLASE GB:CAB62550 FROM [ARABIDOPSIS THALIANA][PUTATIVE] | Decarboxylase |
| 11970 | 1522 | 9-CIS-EPOXYCAROTENOID DIOXYGENASE, PUTATIVE SIMILAR TO 9-CIS-EPOXYCAROTENOID DIOXYGENASE GB:AAF26356 [PHASEOLUS VULGARIS] | Oxygenases |
| 11975 | 1523 | TERPENE SYNTHASE-RELATED PROTEIN, PUTATIVE CONTAINS PFAM PROFILE: PF01397 TERPENE SYNTHASE FAMILY | Synthase |
| 11977 | 1524 | GERANYLGERANYL PYROPHOSPHATE SYNTHETASE, PUTATIVE SIMILAR TO GERANYLGERANYL PYROPHOSPHATE SYNTHETASE GB:P34802 [ARABIDOPSIS THALIANA] | Synthase |
| 11978 | 1525 | TERPENE SYNTHASE GB:CAA72074 FROM [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN SIMILAR TO] | Synthase |
| 11979 | 1526 | GERANYLGERANYL PYROPHOSPHATE SYNTHASE GGPS3 ALMOST IDENTICAL TO GB:S71231 FROM [ARABIDOPSIS THALIANA][PUTATIVE] | Synthase |
| 11980 | 1527 | TERPENE SYNTHASE GB:CAA72074 FROM [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN SIMILAR TO] | Synthase |
| 11981 | 1528 | GERANYLGERANYL PYROPHOSPHATE SYNTHASE GGPS3 ALMOST IDENTICAL TO GB:S71231 FROM [ARABIDOPSIS THALIANA][PUTATIVE] | Synthase |
| 11983 | 1529 | GLUCAN SYNTHASES[HYPOTHETICAL PROTEIN CONTAINS SIMILARITY TO] | Synthase |
| 12004 | 1530 | CALLOSE SYNTHASE CATALYTIC SUBUNIT-LIKE PROTEIN GB:CAB88264 GI:7630056 FROM [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN SIMILAR TO] | Synthase |

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| 12010 | 1531 | RECEPTOR-LIKE SERINE/THREONINE KINASE, PUTATIVE SIMILAR TO RECEPTOR-LIKE SERINE/THREONINE KINASE GB:AAC50043 GI:2465923 FROM [ARABIDOPSIS THALIANA] | Kinase, Protein |
| 12015 | 1532 | DNA-LIGASE ZN-FINGER REGION (REGION ACTS AS A DNA NICK SENSOR) (3 COPIES AT N-TERMINUS) | Ligase |
| 12020 | 1533 | PHOSPHOENOLPYRUVATE CARBOXYLASE (PPC) IDENTICAL TO PHOSPHOENOLPYRUVATE CARBOXYLASE (PPC) GB:AF071788 [ARABIDOPSIS THALIANA] | Carboxylase |
| 12022 | 1534 | GALACTOSYLTRANSFERASE, PUTATIVE CONTAINS PFAM PROFILE: PF01762 GALACTOSYLTRANSFERASE; SIMILAR TO AVR9 ELICITOR RESPONSE PROTEIN. GB:CAA06925 [NICOTIANA TABACUM] | Transferases |
| 12053 | 1535 | PROTEIN PHOSPHATASE TYPE 2C SIMILAR TO PROTEIN PHOSPHATASE TYPE 2C GB:AAD17805 FROM [LOTUS JAPONICUS][PUTATIVE] | Phosphatase |
| 12088 | 1536 | PHOSPHATIDYLINOSITOL 3- AND 4-KINASE HYPOTHETICAL PROTEIN CONTAINS PFAM PROFILE: PF00454 | Kinase |
| 12095 | 1537 | LYSOPHOSPHOLIPASE SIMILAR TO LYSOPHOSPHOLIPASE GB:AAD52700 [SCHISTOSOMA JAPONICUM][PUTATIVE] | Lipase |
| 12099 | 1538 | ACETYL-COA CARBOXYLASE BIOTIN-CONTAINING SUBUNIT SIMILAR TO ACETYL-COA CARBOXYLASE BIOTIN-CONTAINING SUBUNIT GB:AAC49114 [ARABIDOPSIS THALIANA]; CONTAINS PFAM PROFILE: PF00364 BIOTIN-REQUIRING ENZYMES[PUTATIVE] | Carboxylase |
| 12102 | 1539 | POLYGALACTURONASE SIMILAR TO POLYGALACTURONASE GB:BAA88472 [CUCUMIS SATIVUS][PUTATIVE] | Glycosylase |
| 12110 | 1540 | BETA-1,3-GLUCANASE PRECURSOR SIMILAR TO BETA-1,3-GLUCANASE PRECURSOR GB:AAD10386 [ORYZA SATIVA][PUTATIVE] | Glycosylase |
| 12119 | 1541 | PROTEIN KINASE, PUTATIVE SIMILAR TO SOMATIC EMBRYOGENESIS RECEPTOR-LIKE KINASE GB:AAB61708 FROM [DAUCUS CAROTA] | Kinase, Protein |

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| 12124 | 1542 | GLYCOSYL TRANSFERASES GROUP 1, HYPOTHETICAL PROTEIN CONTAINS PFAM PROFILE:PF00534 | Transferases |
| 12133 | 1543 | RECEPTOR KINASE SIMILAR TO RECEPTOR KINASE GB:S70769 FROM [ARABIDOPSIS THALLIANA][PUTATIVE] | Kinase, Protein |
| 12166 | 1544 | LIPASE/HYDROLASE GDSE-LIKE MOTIF; PUTATIVE CONTAINS PFAM PROFILE: PF00657 LIPASE/ACYLHYDROLASE | Lipase |
| 12181 | 1545 | GLUCOSYLTRANSFERASE SIMILAR TO UDP-GLUCOSE GLUCOSYLTRANSFERASE GB:X77459 [MANIHOT ESCULENTA], UDP-GLUCOSE:FLAVONOID GLYCOSYLTRANSFERASE GB:BAA36411 [VIGNA MUNGO][PUTATIVE] | Transferases |
| 12183 | 1546 | SERINE PROTEASE SIMILAR TO HUMAN HTRA SERINE PROTEASE GB:AAC97211 [HOMO SAPIENS][PUTATIVE] | Protease |
| 12184 | 1547 | SERINE PROTEASE SIMILAR TO HUMAN HTRA SERINE PROTEASE GB:AAC97211 [HOMO SAPIENS][PUTATIVE] | Protease |
| 12186 | 1548 | PROTEIN PHOSPHATASE 2C DOMAIN | Phosphatase |
| 12211 | 1549 | PROTEIN PHOSPHATASE, PUTATIVE SIMILAR TO PROTEIN PHOSPHATASE-2C GB:AAC36699 FROM [MESEMBRYANTHEMUM CRYSTALLINUM] | Phosphatase |
| 12216 | 1550 | POLYGALACTURONASE, PUTATIVE SIMILAR TO ENDOPOLYGALACTURONASE GB:225933 FROM [LYCOPERSICON ESCULENTUM] | Glycosylase |
| 12224 | 1551 | ACYL-COA SYNTHETASE, AMP-BINDING PROTEIN, PUTATIVE CONTAINS PFAM PROFILE: PF00501 AMP- BINDING ENZYME; SIMILAR TO ACYL-COA SYNTHETASE GB:CAB54055 [PSEUDOMONAS PUTIDA] | Synthase |
| 12225 | 1552 | CHITINASE BASIC, PUTATIVE SIMILAR TO BASIC CHITINASE GB:CAA78843 [LYCOPERSICON ESCULENTUM] (PLANT MOL. BIOL. 22 (6), 1017-1029 (1993)) | Chitinase |
| 12239 | 1553 | PECTINESTERASE, PUTATIVE SIMILAR TO PECTINESTERASE GB:AAB57669 [CITRUS SINENSIS]; CONTAINS PFAM PROFILE: PF01095 PECTINESTERASE | Esterase |

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| 12240 | 1554 | PEROXIDASE, PUTATIVE SIMILAR TO PEROXIDASE GB:AAD37376 [GLYCINE MAX] | Oxidase |
| 12242 | 1555 | PROTEIN PHOSPHATASE-2C, PUTATIVE SIMILAR TO PROTEIN PHOSPHATASE-2C GB:AAC35951 [MESEMBRYANTHEMUM CRYSTALLINUM]; CONTAINS PFAM PROFILE: PF00481 PROTEIN PHOSPHATASE 2C | Phosphatase |
| 12253 | 1556 | NON-LTR RETROELEMENT REVERSE TRANSCRIPTASES[HYPOTHETICAL PROTEIN SIMILAR TO] | Transcriptase |
| 12260 | 1557 | PROTEIN PHOSPHATASE SIMILAR TO PROTEIN PHOSPHATASE-2C GB:AAC36698 FROM [MESEMBRYANTHEMUM CRYSTALLINUM][PUTATIVE] | Phosphatase |
| 12266 | 1558 | DNA METHYLASE DOMAIN | Methylase |
| 12277 | 1559 | SERINE/THREONINE PROTEIN KINASE, PUTATIVE CONTAINS PFAM PROFILE: PF00069 EUKARYOTIC PROTEIN KINASE DOMAIN | Kinase, Protein |
| 12306 | 1560 | ION CHANNEL PROTEIN FROM [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN CONTAINS SIMILARITY TO] | Channel |
| 12307 | 1561 | ION CHANNEL PROTEIN FROM [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN CONTAINS SIMILARITY TO] | Channel |
| 12309 | 1562 | GLUTAMATE DECARBOXYLASE (GAD) (ERT D1) GB:P54767 [LYCOPERSICON ESCULENTUM]; SIMILAR TO N-TERMINAL PORTION OF | Decarboxylase |
| 12313 | 1563 | GLUTAMATE DECARBOXYLASE, PUTATIVE SIMILAR TO GLUTAMATE DECARBOXYLASE GB:Q07346 [PETUNIA X HYBRIDA] (J. BIOL. CHEM. 268 (26), 19610- 19617 (1993)) | Decarboxylase |
| 12316 | 1564 | ACID PHOSPHATASE TYPE 5 IDENTICAL TO GB:CAB63938 FROM [ARABIDOPSIS THALIANA] | Phosphatase |
| 12333 | 1565 | AMIDASE, PUTATIVE SIMILAR TO AMIDASE GB:AAA26183 FROM [RHODOCOCCLUS SP.] | AMIDASE |

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| 12361 | 1566 | DIACYLGLYCEROL PYROPHOSPHATE PHOSPHATASE, PUTATIVE SIMILAR TO GB:NP_010570 FROM [SACCHAROMYCES CEREVISIAE], CONTAINS PFAM PROFILE: PF01569 PHOSPHATASE PAP2 SUPERFAMILY | Phosphatase |
| 12366 | 1567 | MANDELATE RACEMASE/MUCONATE LACTONIZING ENZYME FAMILY, UNKNOWN PROTEIN CONTAINS PFAM PROFILE: PF01188 | Epimerase |
| 12383 | 1568 | PROTEIN PHOSPHATASE 2B REGULATORY SUBUNIT CALCINEURIN B SUBUNIT GB:P42322 FROM [NAEGLERIA GRUBERI] (GENE 154 (1), 39-45 (1995)) | Phosphatase |
| 12389 | 1569 | ASPARTYL PROTEASE, CHLOROPLAST NUCLEOID DNA-BINDING PROTEIN SIMILAR TO GB:BAA22813 FROM [NICOTIANA TABACUM] (PLANT CELL 9 (9), 1673-1682 (1997)), CONTAINS PFAM PROFILE: PF00026 EUKARYOTIC ASPARTYL PROTEASE[PUTATIVE] | Protease |
| 12410 | 1570 | URIDYLATE KINASE, PUTATIVE SIMILAR TO UMP-KINASE GB:CAB38122 FROM [LACTOCOCCUS LACTIS] | Kinase |
| 12423 | 1571 | PROTEIN KINASE, PUTATIVE SIMILAR TO SOMATIC EMBRYOGENESIS RECEPTOR-LIKE KINASE GB:AAB61708 FROM [DAUCUS CAROTA] | Kinase, Protein |
| 12442 | 1572 | FLAVANONE-3-HYDROXYLASE GB:Q05965 FROM [MATTHIOLA INCANA], CONTAINS PFAM PROFILE: PF00671 IRON/ASCORBATE OXIDOREDUCTASE FAMILY[HYPOTHETICAL PROTEIN CONTAINS SIMILARITY TO] | Hydroxylase |
| 12443 | 1573 | FLAVONOL SYNTHASE (FLS) GB:Q41452 FROM [SOLANUM TUBEROSUM], CONTAINS PFAM PROFILE: PF00671 IRON/ASCORBATE OXIDOREDUCTASE FAMILY[HYPOTHETICAL PROTEIN CONTAINS SIMILARITY TO] | Synthase |
| 12445 | 1574 | PHOSPHOSERINE AMINOTRANSFERASE GB:P19689 FROM [YERSINIA ENTEROCOLITICA][HYPOTHETICAL PROTEIN CONTAINS SIMILARITY TO] | Transferases |
| 12459 | 1575 | TRNA ISOPENTENYL TRANSFERASE, PUTATIVE SIMILAR TO TRNA ISOPENTENYL TRANSFERASE GB:AAF00582 FROM [ARABIDOPSIS THALIANA] | Transferases |

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| 12471 | 1576 | FUCOSYLTRANSFERASE, PUTATIVE SIMILAR TO FUCT C3 PROTEIN GB:CAB52254 FROM [VIGNA RADIATA] (J. BIOL. CHEM. (1999) 274 (31), 21830-21839) | Transferases |
| 12488 | 1577 | CINNAMYL ALCOHOL DEHYDROGENASE IDENTICAL TO GB:P48523 FROM [ARABIDOPSIS THALIANA] | Dehydrogenases |
| 12501 | 1578 | AMINO ACID PERMEASE, PUTATIVE, 5' PARTIAL CONTAINS PFAM PROFILE: PF00324 AMINO ACID PERMEASE | Transporter |
| 12508 | 1579 | BETA-XYLOSIDASE, PUTATIVE SIMILAR TO BETA-XYLOSIDASE A GB:BAA28267 FROM [ASPERGILLUS ORYZAE] | Glycosylase |
| 12516 | 1580 | RECEPTOR-LIKE PROTEIN KINASE, PUTATIVE SIMILAR TO LEUCINE-RICH RECEPTOR-LIKE PROTEIN KINASE GB:AAC36318 FROM [MALUS DOMESTICA] | Kinase, Protein |
| 12564 | 1581 | GERANYL GERANYL PYROPHOSPHATE SYNTHASE, PUTATIVE SIMILAR TO GERANYL GERANYL PYROPHOSPHATE SYNTHASE GB:BAA23157 [ARABIDOPSIS THALIANA] | Synthase |
| 12567 | 1582 | RECEPTOR KINASE PROTEIN, PUTATIVE SIMILAR TO RECEPTOR KINASE GB:AAA33715 [PETUNIA INTEGRIFOLIA] | Kinase, Protein |
| 12572 | 1583 | MITOCHONDRIAL CARRIER PROTEIN, PUTATIVE CONTAINS PFAM PROFILE: PF00153 MITOCHONDRIAL CARRIER PROTEINS | Transporter |
| 12597 | 1584 | TETRAACYLDISACCHARIDE 4'-KINASE GB:P27300 [ESCHERICHIA COLI][HYPOTHETICAL PROTEIN SIMILAR TO] | Kinase |
| 12599 | 1585 | PURPLE ACID PHOSPHATASE, PUTATIVE SIMILAR TO PURPLE ACID PHOSPHATASE GB:CAA06921 [IPOMOEA BATATAS] | Phosphatase |
| 12602 | 1586 | PROTEIN KINASE, PUTATIVE CONTAINS PFAM PROFILE: PF00069 EUKARYOTIC PROTEIN KINASE DOMAIN | Kinase, Protein |
| 12627 | 1587 | DNA TOPOISOMERASE VI SUBUNIT B TYPE II GB:O05207 FROM [SULFOLOBUS SHIBATAE], UNKNOWN PROTEIN SIMILAR TO | Isomerase |

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| 12662 | 1588 | PHOSPHORIBOSYAMIDOIMIDAZOLE-SUCCINOCARBOXAMIDE SYNTHASE, PUTATIVE SIMILAR TO PHOSPHORIBOSYLAMIDOIMIDAZOLE-SUCCINOCARBOXAMIDE SYNTHASE GB:P38025 FROM [ARABIDOPSIS THALIANA] | Synthase |
| 12676 | 1589 | ABC TRANSPORTER GB:AAC49791 FROM [ARABIDOPSIS THALIANA], SIMILAR TO MRP-LIKE | Transporter |
| 12685 | 1590 | SERINE/THREONINE-SPECIFIC PROTEIN KINASE, PUTATIVE SIMILAR TO SERINE/THREONINE-SPECIFIC PROTEIN KINASE GB:T02731 FROM [ARABIDOPSIS THALIANA] | Kinase, Protein |
| 12693 | 1591 | IRON/ASCORBATE OXIDOREDUCTASE FAMILY | Reductase |
| 12696 | 1592 | PROTEIN KINASE DOMAIN | Kinase, Protein |
| 12698 | 1593 | ADENYL CYCLASE, PUTATIVE, 3' PARTIAL SIMILAR TO ADENYL CYCLASE GB:AAB87670 FROM [NICOTIANA TABACUM] | Cyclase |
| 12699 | 1594 | ADENYL CYCLASE, PUTATIVE, 5' PARTIAL SIMILAR TO ADENYL CYCLASE GB:AAB87670 [NICOTIANA TABACUM] | Cyclase |
| 12703 | 1595 | 1-D-DEOXYXYLULOSE 5-PHOSPHATE SYNTHASE, PUTATIVE SIMILAR TO 1-D-DEOXYXYLULOSE 5-PHOSPHATE SYNTHASE GB:AAD38941 [LYCOPERSICON ESCULENTUM] | Synthase |
| 12709 | 1596 | UDP-GLUCOSE:INDOLE-3-ACETATE BETA-D-GLUCOSYLTRANSFERASE, PUTATIVE SIMILAR TO UDP-GLUCOSE:INDOLE-3-ACETATE BETA-D-GLUCOSYLTRANSFERASE GB:AAB58497 | Transferases |
| 12717 | 1597 | PEPTIDYL-PROLYL CIS-TRANS ISOMERASE FKBP-TYPE, PUTATIVE CONTAINS PFAM PROFILE: PF00254 FKBP-TYPE PEPTIDYL-PROLYL CIS-TRANS ISOMERASES | Isomerase |
| 12728 | 1598 | UDP-GLUCOSE GLUCOSYLTRANSFERASE SIMILAR TO GB:Q40284 FROM [MANIHOT ESCULENTA][PUTATIVE] | Transferases |
| 12729 | 1599 | UDP-GLUCOSE GLUCOSYLTRANSFERASE SIMILAR TO GB:Q40284 FROM [MANIHOT ESCULENTA][PUTATIVE] | Transferases |

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| 12730 | 1600 | PEROXIDASE ALMOST IDENTICAL TO GB:CAA66965 AND GB:CAA67360 FROM [ARABIDOPSIS THALIANA][PUTATIVE] | Oxidase |
| 12731 | 1601 | UDP-GLUCOSE GLUCOSYLTRANSFERASE SIMILAR TO GB:Q40284 FROM [MANIHOT ESCULENTA][PUTATIVE] | Transferases |
| 12732 | 1602 | UDP-GLUCOSE GLUCOSYLTRANSFERASE SIMILAR TO GB:Q40284 FROM [MANIHOT ESCULENTA][PUTATIVE] | Transferases |
| 12733 | 1603 | UDP-GLUCOSE GLUCOSYLTRANSFERASE SIMILAR TO GB:Q40284 FROM [MANIHOT ESCULENTA][PUTATIVE] | Transferases |
| 12749 | 1604 | SALICYLIC ACID CARBOXYL METHYLTRANSFERASE, PUTATIVE SIMILAR TO GB:AAF00108 FROM [CLARKIA BREWERI] | Transferases |
| 12792 | 1605 | ALTERNATIVE OXIDASE 1B PRECURSOR IDENTICAL TO GB:O23913 FROM [ARABIDOPSIS THALIANA] | Oxidase |
| 12793 | 1606 | ALTERNATIVE OXIDASE 1A PRECURSOR IDENTICAL TO GB:Q39219 FROM [ARABIDOPSIS THALIANA] | Oxidase |
| 12813 | 1607 | ACETYLTRANSFERASE (GNAT) FAMILY; HYPOTHETICAL PROTEIN PREDICTED BY GENEMARK.HMM, CONTAINS PFAM PROFILE:PF00583 ACETYLTRANSF | Transferases |
| 12849 | 1608 | DNA-DIRECTED RNA POLYMERASE II 19 KD POLYPEPTIDE (SUBUNIT 5) GB:P46279 [GLYCINE MAX][HYPOTHETICAL PROTEIN SIMILAR TO] | Polymerase |
| 12875 | 1609 | ETHYLENE RECEPTOR, PUTATIVE (ETR2) SIMILAR TO ETHYLENE RECEPTOR HOMOLOG GB:AAD31396 FROM [LYCOPERSICON ESCULENTUM], CONTAINS PFAM PROFILE: PF01590 GAF DOMAIN | Receptor |
| 12897 | 1610 | PROTEIN PHOSPHATASE GB:AAD17805 FROM [LOTUS JAPONICUS] | Phosphatase |
| 12902 | 1611 | GMC OXIDOREDUCTASE DOMAIN | Reductase |
| 12910 | 1612 | CYANATE LYASE (CYN) IDENTICAL TO CYANASE (CYN) GB:AB004568 [ARABIDOPSIS THALIANA] | Lyase |
| 12918 | 1613 | DIENELACTONE HYDROLASE FAMILY | Hydrolase |
| 12921 | 1614 | DIENELACTONE HYDROLASE FAMILY | Hydrolase |

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| 12922 | 1615 | DUAL-SPECIFICITY PROTEIN PHOSPHATASE IDENTICAL TO DSPTP1 PROTEIN GB:CAA77232 FROM [ARABIDOPSIS THALIANA] | Phosphatase |
| 12924 | 1616 | IPP TRANSFERASE, HYPOTHETICAL PROTEIN CONTAINS PFAM PROFILE: PF01715 | Transferases |
| 12926 | 1617 | PROTEIN KINASE GB:AAD24596 FROM [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN SIMILAR TO][PUTATIVE] | Kinase, Protein |
| 12934 | 1618 | XYLOGLUCAN ENDOTRANSGLYCOSYLASE, PUTATIVE SIMILAR TO XYLOGLUCAN ENDOTRANSGLYCOSYLASE 1 GB:CAA10231 FROM [FAGUS SYLVATICA] (PLANT PHYSIOL.(1999) 119, 1148-1148) | Glycosylase |
| 12936 | 1619 | RECEPTOR-LIKE KINASE, PUTATIVE SIMILAR TO TMK GB:CAA69028 FROM [ORYZA SATIVA] | Kinase, Protein |
| 12938 | 1620 | BETA-1,3-GLUCANASE, PUTATIVE SIMILAR TO BETA-1,3-GLUCANASE GB:BAA89481 FROM [SALIX GILGIANA] | Glycosylase |
| 12943 | 1621 | NAD DEPENDENT EPIMERASE, PUTATIVE CONTAINS PFAM PROFILE: PF01370 NAD DEPENDENT EPIMERASE/DEHYDRATASE FAMILY | Dehydratase |
| 12953 | 1622 | BETA-AMYLASE, PUTATIVE SIMILAR TO BETA-AMYLASE GB:CAB58423 [ARABIDOPSIS THALIANA] | Glycosylase |
| 12955 | 1623 | DIHYDROXYACID DEHYDRATASE, PUTATIVE SIMILAR TO DIHYDROXYACID DEHYDRATASE GB:CAA60939 [SACCHAROMYCES CEREVISIAE] | Dehydratase |
| 12964 | 1624 | HYDROXYETHYLTHIAZOLE KINASE, PUTATIVE SIMILAR TO HYDOXYETHYLTHIAZOLE KINASE (THIM) GB:BAA76743 [ESCHERICHIA COLI] | Kinase |
| 12965 | 1625 | MUCIN CORE 2 BETA 6-N-ACETYLGLUCOSAMINYLTRANSFERASE GB:AAA83244 [BOS TAURUS][HYPOTHETICAL PROTEIN SIMILAR TO] | Transferases |
| 12974 | 1626 | PECTINESTERASE, PUTATIVE CONTAINS PFAM PROFILE: PF01095 PECTINESTERASE | Esterase |

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| 12983 | 1627 | 9-CIS-EPOXYCAROTENOID DIOXYGENASE, PUTATIVE SIMILAR TO GB:CAB10168 FROM [LYCOPERSICON ESCULENTUM] (J. EXP. BOT. 47, 2111-2112 (1997)) | Oxygenases |
| 12984 | 1628 | PECTATE LYASE, PUTATIVE SIMILAR TO GB:AAF19196 FROM [MUSA ACUMINATA] | Lyase |
| 12986 | 1629 | RECEPTOR KINASE, PUTATIVE SIMILAR TO CLV1 RECEPTOR KINASE GB:AAB58929 FROM [ARABIDOPSIS THALIANA] | Kinase, Protein |
| 12988 | 1630 | NON-LTR RETROELEMENT REVERSE TRANSCRIPTASE GB:AAC63678 GI:3738337 FROM [ARABIDOPSIS THALIANA], HYPOTHETICAL PROTEIN, 3' PARTIAL SIMILAR TO PUTATIVE | Transcriptase |
| 12996 | 1631 | BETA-1,3-GLUCANASE, PUTATIVE SIMILAR TO BETA- 1,3-GLUCANASE GB:BAA89481 FROM [SALIX GILGIANA] | Glycosylase |
| 13003 | 1632 | PROTEIN KINASE, PUTATIVE SIMILAR TO PROTEIN KINASE GB:BAA24694 FROM [ARABIDOPSIS THALIANA] | Kinase, Protein |
| 13005 | 1633 | ALPHA/BETA HYDROLASE FOLD | Hydrolase |
| 13017 | 1634 | PROTEIN KINASE, PUTATIVE SIMILAR TO GB:BAA24694 FROM [ARABIDOPSIS THALIANA] (PLANT CELL PHYSIOL. 38 (3), 248-258 (1997)) | Kinase, Protein |
| 13018 | 1635 | PROTEIN KINASE, PUTATIVE SIMILAR TO GB:BAA24694 FROM [ARABIDOPSIS THALIANA] (PLANT CELL PHYSIOL. 38 (3), 248-258 (1997)) | Kinase, Protein |
| 13022 | 1636 | PROCESSING PEPTIDASE, CHLOROPLAST THYLAKOIDAL PROCESSING PEPTIDASE, PUTATIVE SIMILAR TO GB:CAA71502 FROM [ARABIDOPSIS THALIANA] | Protease |
| 13029 | 1637 | KINASE-LIKE PROTEIN TMKL1 PRECURSOR IDENTICAL TO PUTATIVE KINASE-LIKE PROTEIN TMKL1 PRECURSOR GB:P33543 FROM [ARABIDOPSIS THALIANA], (PLANT MOL. BIOL. 23 (2), 415-421 (1993))[PUTATIVE] | Kinase, Protein |
| 13030 | 1638 | PECTATE LYASE, PUTATIVE SIMILAR TO PECTATE LYASE GB:AAB71208 FROM [FRAGARIA ANANASSA], (PLANT MOL. BIOL. 34 (6), 867-877 (1997)) | Lyase |

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| 13034 | 1639 | NADPH-FERRIHEMOPROTEIN REDUCTASE GB:AAF02110 FROM [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN SIMILAR TO][PUTATIVE] | Reductase |
| 13043 | 1640 | PROTEIN KINASE, PUTATIVE SIMILAR TO PROTEIN KINASE GB:BAA24694 FROM [ARABIDOPSIS THALIANA] | Kinase, Protein |
| 13061 | 1641 | ENDOXYLOGLUCAN TRANSFERASE, PUTATIVE SIMILAR TO GB:C49539 FROM [ARABIDOPSIS THALIANA] (J. BIOL. CHEM. 268 (34), 25364-25368 (1993)) | Transferases |
| 13067 | 1642 | ACYL-(ACYL CARRIER PROTEIN) THIOESTERASE IDENTICAL TO ACYL-(ACYL CARRIER PROTEIN) THIOESTERASE GB:Z36912 [ARABIDOPSIS THALIANA] (ARCH. BIOCHEM. BIOPHYS. 316 (1), 612-618 (1995)) | Esterase |
| 13070 | 1643 | GLYCOSYL TRANSFERASE, PUTATIVE CONTAINS PFAM PROFILE: PF01501 GLYCOSYL TRANSFERASE FAMILY 8 | Transferases |
| 13084 | 1644 | REVERSE TRANSCRIPTASE GB:S65812 [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN SIMILAR TO] | Transcriptase |
| 13085 | 1645 | NITRATE TRANSPORTER, PUTATIVE SIMILAR TO NITRATE TRANSPORTER (NTL1) GB:AAC28086 [ARABIDOPSIS THALIANA] | Transporter |
| 13088 | 1646 | BILE ACID SODIUM SYMPORTER FAMILY | Transporter |
| 13096 | 1647 | WALL-ASSOCIATED SERINE/THREONINE KINASE, PUTATIVE SIMILAR TO WALL-ASSOCIATED KINASE 4 GB:CAA08793 FROM [ARABIDOPSIS THALIANA] | Kinase, Protein |
| 13103 | 1648 | SOMATIC EMBRYOGENESIS RECEPTOR-LIKE KINASE, PUTATIVE SIMILAR TO SOMATIC EMBRYOGENESIS RECEPTOR-LIKE KINASE GB:AAB61708 FROM [DAUCUS CAROTA] | Kinase, Protein |
| 13129 | 1649 | TERPENE SYNTHASE-RELATED PROTEIN CONTAINS PFAM PROFILE: PF01397 TERPENE SYNTHASE FAMILY | Synthase |
| 13130 | 1650 | TERPENE SYNTHASE-RELATED PROTEIN CONTAINS PFAM PROFILE: PF01397 TERPENE SYNTHASE FAMILY | Synthase |

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| 13131 | 1651 | LIMONENE CYCLASE, PUTATIVE, 5' PARTIAL SIMILAR TO LIMONENE CYCLASE GB:BAA08367 FROM [PERILLA FRUTESCENS] | Cyclase |
| 13132 | 1652 | LIMONENE CYCLASE, PUTATIVE SIMILAR TO LIMONENE CYCLASE GB:BAA08367 FROM [PERILLA FRUTESCENS], CONTAINS PFAM PROFILE: PF01397 TERPENE SYNTHASE FAMILY | Synthase |
| 13165 | 1653 | CELLULASE, PUTATIVE CONTAINS PFAM PROFILE: PF00150 CELLULASE (GLYCOSYL HYDROLASE FAMILY 5) | Hydrolase |
| 13166 | 1654 | CELLULASE, PUTATIVE CONTAINS PFAM PROFILE: PF00150 CELLULASE (GLYCOSYL HYDROLASE FAMILY 5) | Hydrolase |
| 13190 | 1655 | ALPHA GALACTOSIDASE GB:AAA73963 [GLYCINE MAX}, UNKNOWN PROTEIN SIMILAR TO | Glycosylase |
| 13214 | 1656 | POLYGALACTURONASE, PUTATIVE SIMILAR TO POLYGALACTURONASE (PG1) GB:AAD46483 [GLYCINE MAX] | Glycosylase |
| 13226 | 1657 | PROTEIN KINASE, PUTATIVE CONTAINS PFAM PROFILE: PF00069 EUKARYOTIC PROTEIN KINASE DOMAIN | Kinase, Protein |
| 13228 | 1658 | ALPHA-MANNOSIDASE, PUTATIVE SIMILAR TO LYSOSOMAL ALPHA-MANNOSIDASE GB:AAC34130 [HOMO SAPIENS] (HUM. MOL. GENET. 6 (5), 717-726 (1997)) | Glycosylase |
| 13234 | 1659 | SHORT CHAIN ALCOHOL DEHYDROGENASE CONTAINS PFAM PROFILE: PF00106 SHORT CHAIN DEHYDROGENASE; SIMILAR TO SEX DETERMINATION PROTEIN TASSELSEED 2 GB:P50160 [ZEA MAYS][PUTATIVE] | Dehydrogenase |
| 13235 | 1660 | SHORT CHAIN ALCOHOL DEHYDROGENASE CONTAINS PFAM PROFILE: PF00106 SHORT CHAIN DEHYDROGENASE; SIMILAR TO SEX DETERMINATION PROTEIN TASSELSEED 2 GB:P50160 [ZEA MAYS][PUTATIVE] | Dehydrogenase |
| 13240 | 1661 | ALPHA/BETA HYDROLASE FOLD | Hydrolase |

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| 13248 | 1662 | SHIKIMATE KINASE SIMILAR TO SHIKIMATE KINASE PRECURSOR GB:CAA45121 [LYCOPERSICON ESCULENTUM][PUTATIVE] | Kinase |
| 13254 | 1663 | PROTEIN KINASE, PUTATIVE SIMILAR TO PROTEIN KINASE APK1A GB:Q06548 FROM [ARABIDOPSIS THALIANA] | Kinase, Protein |
| 13271 | 1664 | PEPTIDASE FAMILY M48 | Protease |
| 13274 | 1665 | PROTEIN PHOSPHATASE 2C, PUTATIVE SIMILAR TO PROTEIN PHOSPHATASE 2C GB:T09640 FROM [MEDICAGO SATIVA] | Phosphatase |
| 13292 | 1666 | ESTERASE, PUTATIVE SIMILAR TO ESTERASE HDE GB:BAA82510 FROM [PETROLEUM-DEGRADING BACTERIUM HD-1] | Esterase |
| 13302 | 1667 | PECTATE LYASE, PUTATIVE SIMILAR TO PECTATE LYASE GB:CAA70735 [ZINNIA ELEGANS] (PLANT J. 13 (1), 17-28 (1998)); CONTAINS PFAM PROFILE: PF00544 PECTATE LYASE | Lyase |
| 13326 | 1668 | ALTERNATIVE OXIDASE 1C PRECURSOR IDENTICAL TO ALTERNATIVE OXIDASE 1C PRECURSOR GB:O22048 FROM [ARABIDOPSIS THALIANA] | Oxidase |
| 13355 | 1669 | NADPH:QUINONE OXIDOREDUCTASE (NQR) NEARLY IDENTICAL TO NADPH:QUINONE OXIDOREDUCTASE (NQR) GB:AF145234 [ARABIDOPSIS THALIANA] | Reductase |
| 13365 | 1670 | EXONUCLEASE | Nuclease |
| 13366 | 1671 | PECTIN METHYLESTERASE, PUTATIVE SIMILAR TO PECTIN METHYLESTERASE GB:AAB38794 FROM [LYCOPERSICON ESCULENTUM] | Esterase |
| 13372 | 1672 | PROTEIN KINASE DOMAIN LRR | Kinase, Protein |
| 13385 | 1673 | NON-LTR REVERSE TRANSCRIPTASE, PUTATIVE SIMILAR TO GB:S65812 FROM [ARABIDOPSIS THALIANA] AND OTHER PUTATIVE NON-LTR REVERSE TRANSCRIPTASES | Transcriptase |
| 13389 | 1674 | PEROXIDASE, PUTATIVE SIMILAR TO PEROXIDASE ATP26A GB:CAA72487 GI:1890317 [ARABIDOPSIS THALIANA] | Oxidase |

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| 13394 | 1675 | BETA-1,3 GLUCANASE GB:CAB85903 GI:7414433 [PISUM SATIVUM][HYPOTHETICAL PROTEIN SIMILAR TO] | Glycosylase |
| 13417 | 1676 | RECEPTOR KINASE, PUTATIVE SIMILAR TO RECEPTOR KINASE GB:AAD02501 FROM [ARABIDOPSIS THALIANA] | Kinase, Protein |
| 13420 | 1677 | PROLYL 4-HYDROXYLASE, PUTATIVE SIMILAR TO PROLYL 4-HYDROXYLASE ALPHA SUBUNIT PRECURSOR GB:Q10576 FROM [CAENORHABDITIS ELEGANS] | Hydroxylase |
| 13421 | 1678 | PROLYL 4-HYDROXYLASE, PUTATIVE SIMILAR TO PROLYL 4-HYDROXYLASE ALPHA SUBUNIT PRECURSOR GB:Q10576 FROM [CAENORHABDITIS ELEGANS] | Hydroxylase |
| 13424 | 1679 | AAA-TYPE ATPASE GB:AAD31347 GI:4874284 FROM [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN SIMILAR TO][PUTATIVE] | ATPase |
| 13441 | 1680 | PROTEIN KINASE, PUTATIVE SIMILAR TO PROTEIN KINASE APK1A GB:Q06548 FROM [ARABIDOPSIS THALIANA] | Kinase, Protein |
| 13485 | 1681 | PECTINESTERASE SIMILAR TO PECTINESTERASE PRECURSOR GB:Q43043 [PETUNIA INTEGRIFOLIA]; CONTAINS PFAM PROFILE: PF01095 PECTINESTERASE[PUTATIVE] | Esterase |
| 13486 | 1682 | VESICLE TRANSPORT PROTEIN SIMILAR TO V-SNARE ATVTI1A GB:AAF24061 [ARABIDOPSIS THALIANA][PUTATIVE] | Transporter |
| 13487 | 1683 | TERPENE SYNTHASE-RELATED PROTEIN CONTAINS PFAM PROFILE: PF01397 TERPENE SYNTHASE FAMILY; SIMILAR TO EPIDERMAL GERMACRENE C SYNTHASE GB:AAC39431 [LYCOPERSICON ESCULENTUM],. (+)- DELTA-CADINENE SYNTHASE GB:P93665 [GOSSYPIMUM HIRSUTUM][PUTATIVE] | Synthase |
| 13496 | 1684 | TERPENE SYNTHASE-RELATED PROTEIN CONTAINS PFAM PROFILE: PF01397 TERPENE SYNTHASE FAMILY | Synthase |
| 13497 | 1685 | CHORISMATE MUTASE IDENTICAL TO CHORISMATE MUTASE GB:Z26519 [ARABIDOPSIS THALIANA] | Mutase |

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| 13502 | 1686 | SHORT-CHAIN ALCOHOL DEHYDROGENASE, PUTATIVE SIMILAR TO SHORT-CHAIN ALCOHOL DEHYDROGENASE GB:AAF04194 [PISUM SATIVUM]; CONTAINS PFAM PROFILE: PF00106 SHORT CHAIN DEHYDROGENASE | Dehydrogenase |
| 13503 | 1687 | SHORT-CHAIN ALCOHOL DEHYDROGENASE, PUTATIVE SIMILAR TO SHORT-CHAIN ALCOHOL DEHYDROGENASE GB:AAF04194 [PISUM SATIVUM]; CONTAINS PFAM PROFILE: PF00106 SHORT CHAIN DEHYDROGENASE | Dehydrogenase |
| 13519 | 1688 | TERPENE SYNTHASE, PUTATIVE SIMILAR TO TERPENE SYNTHASE GB:CAA72074 FROM [ARABIDOPSIS THALIANA], CONTAINS PFAM PROFILE: PF01397 TERPENE SYNTHASE FAMILY | Synthase |
| 13520 | 1689 | FARNESYLTRANSFERASE, PUTATIVE (FRAGMENT) FRAGMENT SIMILAR TO FARNESYLTRANSFERASE PRECURSOR GB:T10452 FROM [SINAPIS ALBA] | Transferases |
| 13521 | 1690 | GERANYLGERANYL PYROPHOSPHATE SYNTHASE, PUTATIVE SIMILAR TO GERANYLGERANYL PYROPHOSPHATE SYNTHASE, CHLOROPLAST PRECURSOR GB:P34802 FROM [ARABIDOPSIS THALIANA] | Synthase |
| 13532 | 1691 | ANTHOCYANIN 5-AROMATIC ACYLTRANSFERASE, PUTATIVE SIMILAR TO ANTHOCYANIN 5-AROMATIC ACYLTRANSFERASE GB:BAA74428 FROM [GENTIANA TRIFLORA] | Transferases |
| 13536 | 1692 | FLAVONOL 3-O-GLUCOSYLTRANSFERASE, PUTATIVE SIMILAR TO FLAVONOL 3-O-GLUCOSYLTRANSFERASE GB:Q43716 FROM [PETUNIA X HYBRIDA] | Transferases |
| 13541 | 1693 | ANTHOCYANIN 5-AROMATIC ACYLTRANSFERASE, PUTATIVE SIMILAR TO ANTHOCYANIN 5-AROMATIC ACYLTRANSFERASE GB:BAA74428 [GENTIANA TRIFLORA] | Transferases |

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| 13542 | 1694 | ANTHOCYANIN 5-AROMATIC ACYLTRANSFERASE, PUTATIVE SIMILAR TO ANTHOCYANIN 5-AROMATIC ACYLTRANSFERASE GB:BAA74428 [GENTIANA TRIFLORA] | Transferases |
| 13554 | 1695 | ALPHA/BETA HYDROLASE, PUTATIVE CONTAINS PFAM PROFILE: PF00561 ALPHA/BETA HYDROLASE FOLD | Hydrolase |
| 13563 | 1696 | PHYTOCHELATIN SYNTHETASE GB:CAA07251 FROM [ARABIDOPSIS THALIANA] (PLANT PHYSIOL. 117, 1526-1526 (1998)), UNKNOWN PROTEIN SIMILAR TO PUTATIVEE | Synthase |
| 13564 | 1697 | NON-LTR RETROELEMENT REVERSE TRANSCRIPTASE GB:AAD22368 FROM [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN CONTAINS SIMILARITY TO][PUTATIVE] | Transcriptase |
| 13576 | 1698 | FRUCTOSE-6-PHOSPHATE 2-KINASE/FRUCTOSE-2,6-BISPHOSPHATASE GB:AAF04293, HYPOTHETICAL PROTEIN CONTAINS REGIONS SIMILAR TO | Phosphatase |
| 13584 | 1699 | DEACETYL VINDOLINE 4-O-ACETYLTRANSFERASE, PUTATIVE SIMILAR TO GB:AAC99311 FROM [CATHARANTHUS ROSEUS] (PLANT J. 14 (6), 703-713 (1998)) | Transferases |
| 13595 | 1700 | AMINO ACID TRANSPORTER; UNKNOWN PROTEIN CONTAINS PFAM PROFILE: PF01490 TRANSMEMBRANE AMINO ACID TRANSPORTER PROTEIN | Transporter |
| 13612 | 1701 | BETA-MANNAN ENDOHYDROLASE SIMILAR TO (1-4)-BETA-MANNAN ENDOHYDROLASE GB:AAB87859 FROM [LYCOPERSICON ESCULENTUM][PUTATIVE] | Hydrolase |
| 13665 | 1702 | VETISPIRADIENE SYNTHASE, PUTATIVE, 5' PARTIAL SIMILAR TO VETISPIRADIENE SYNTHASE GB:BAB02386 GI:9294376 FROM [ARABIDOPSIS THALIANA] | Synthase |
| 13685 | 1703 | TERPENE SYNTHASE, PUTATIVE CONTAINS PFAM PROFILE: PF01397 TERPENE SYNTHASE FAMILY | Synthase |

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| 13686 | 1704 | GERANYLGERANYL PYROPHOSPHATE SYNTHASE, PUTATIVE SIMILAR TO GB:P34802 FROM [ARABIDOPSIS THALIANA] (PLANT PHYSIOL. 104 (4), 1469-1470 (1994)) | Synthase |
| 13695 | 1705 | NON-LTR REVERSE TRANSCRIPTASE, PUTATIVE | Transcriptase |
| 13755 | 1706 | PECTIN METHYLESTERASE [PUTATIVE] | Esterase |
| 13796 | 1707 | PEROXIDASE - LYCOPERSICON ESCULENTUM, PIR:S32768[PUTATIVE] | Oxidase |
| 13824 | 1708 | ARABINOSE KINASE - LIKE PROTEIN PUTATIVE ARABINOSE KINASE ISA1, ARABIDOPSIS THALIANA, EMBL:ATY14404 | Kinase |
| 13827 | 1709 | RECEPTOR PROTEIN KINASE -LIKE PROTEIN RECEPTOR-LIKE PROTEIN KINASE PRK1, LYCOPERSICON ESCULENTUM, PIR:T07865 | Kinase, Protein |
| 13834 | 1710 | POLYGALACTURONASE -LIKE PROTEIN POLYGALACTURONASE, MUSKMELON, PIR:T08213 | Glycosylase |
| 13835 | 1711 | ALCOHOL DEHYDROGENASE (ATA1) | Dehydrogenases |
| 13858 | 1712 | SUCROSE SYNTHASE -LIKE PROTEIN SUCROSE SYNTHASE (SUCROSE-UDP GLUCOSYLTRANSFERASE), ARABIDOPSIS THALINA, SWISSPROT:SUS1_ARATH | Synthase |
| 13866 | 1713 | PECTINESTERASE -LIKE PROTEIN PECTINESTERASE PPE8B PRECURSOR, PRUNUS PERSICA, SWISSPROT:PME_PRUPE | Esterase |
| 13868 | 1714 | GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE, EQUUS CABALLUS, EMBL:AF097179[PUTATIVE] | Dehydrogenases |
| 13906 | 1715 | AMINE OXIDASE -LIKE PROTEIN AMINE OXIDASE, CANAVALIA LINEATA, EMBL:AF172681 | Oxidase |
| 13918 | 1716 | TRANSPORTER-LIKE PROTEIN MULTIDRUG-EFFLUX TRANSPORTER BLT, BACILLUS SUBTILIS, PIR:I39792 | Transporter |
| 13919 | 1717 | GLUTATHIONE TRANSFERASE-LIKE PROTEIN GLUTATHIONE TRANSFERASE, PAPAYA, PIR:T09781 | Transferases |
| 13921 | 1718 | AMINE OXIDASE, CANAVALIA LINEATA, EMBL:AF172681[PUTATIVE] | Oxidase |
| 13991 | 1719 | TRIACYLGLYCEROL LIPASE, PSYCHROBACTER IMMOBILIS, PIR:S57275[PUTATIVE] | Lipase |

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| 14001 | 1720 | TYROSINE-PHOSPHATASE-LIKE PROTEIN PROTEIN- TYROSINE-PHOSPHATASE - SCHIZOSACCHAROMYCES POMBE, PIR:A55446 | Phosphatase |
| 14011 | 1721 | PREPHENATE DEHYDRATASE CHLOROPLAST SIMILAR TO BACTERIAL PHEA GENE PRODUCTS[PUTATIVE] | Dehydratase |
| 14014 | 1722 | HISTONE DEACETYLASE SIMILAR TO MAIZE NUCLEOLAR HISTONE DEACETYLASE (U82815) [PUTATIVE] | |
| 14022 | 1723 | PHOSPHATIDYLCHOLINE--STEROL O- ACYLTRANSFERASE (EC 2.3.1.43) PRECURSOR, MOUSE, PIR:XXMSN[PUTATIVE] | Transferases |
| 14023 | 1724 | PROTEINKINASE ATPP -LIKE PROTEIN ATPP PROTEIN, BRASSICA NAPUS, EMBL:BNA245479 | Kinase, Protein |
| 14029 | 1725 | MEMBRANE ION ANTIporter, AMYCOLATOPSIS ORIENTALIS, EMBL:AL078635[PUTATIVE] | Transporter |
| 14030 | 1726 | MEMBRANE ION ANTIporter, AMYCOLATOPSIS ORIENTALIS, EMBL:AL078635[PUTATIVE] | Transporter |
| 14031 | 1727 | MEMBRANE ION ANTIporter, AMYCOLATOPSIS ORIENTALIS, EMBL:AL078635[PUTATIVE] | Transporter |
| 14032 | 1728 | MEMBRANE ION ANTIporter, AMYCOLATOPSIS ORIENTALIS, EMBL:AL078635[PUTATIVE] | Transporter |
| 14038 | 1729 | XYLOGLUCAN ENDO-TRANSGLYCOSYLASE | Glycosylase |
| 14045 | 1730 | HIGH-AFFINITY NITRATE TRANSPORTER - LIKE PROTEIN HIGH-AFFINITY NITRATE TRANSPORTER ACH1, ARABIDOPSIS THALIANA, EMBL:AF019748 | Transporter |
| 14048 | 1731 | 2-PHOSPHOGLYCERATE KINASE - METHANOCOCCUS JANNASCHII, PIR:A64485[PUTATIVE] | Kinase |
| 14072 | 1732 | RECEPTOR-LIKE PROTEIN KINASE RECEPTOR LIKE PROTEIN KINASE LRK1 - ARABIDOPSIS THALIANA,EMBL:ATLECGENE | Kinase, Protein |
| 14078 | 1733 | RECEPTOR-LIKE PROTEIN KINASE RECEPTOR LIKE PROTEIN KINASE LRK1 - ARABIDOPSIS THALIANA, EMBL:ATLECGENE | Kinase, Protein |

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| 14080 | 1734 | RECEPTOR-LIKE PROTEIN KINASE RECEPTOR LIKE PROTEIN KINASE LRK1 - ARABIDOPSIS THALIANA, EMBL:ATLECGENE | Kinase, Protein |
| 14081 | 1735 | RECEPTOR-LIKE PROTEIN KINASE RECEPTOR LIKE PROTEIN KINASE LRK1 - ARABIDOPSIS THALIANA, EMBL:ATLECGENE | Kinase, Protein |
| 14082 | 1736 | RECEPTOR LIKE PROTEIN KINASE RECEPTOR LIKE PROTEIN KINASE LRK1 - ARABIDOPSIS THALIANA, EMBL:ATLECGENE | Kinase, Protein |
| 14083 | 1737 | RECEPTOR LIKE PROTEIN KINASE RECEPTOR LIKE PROTEIN KINASE LRK1 - ARABIDOPSIS THALIANA, EMBL:ATLECGENE | Kinase, Protein |
| 14098 | 1738 | TRNA INTRON ENDONUCLEASE - ARABIDOPSIS THALIANA, EMBL:AB036339[PUTATIVE] | Nuclease |
| 14104 | 1739 | TRANSPORTER PROTEIN[PUTATIVE] | Transporter |
| 14105 | 1740 | TRANSPORTER PROTEIN[PUTATIVE] | Transporter |
| 14106 | 1741 | PROTEIN KINASE NPK1-RELATED PROTEIN KINASE 2 - ARABIDOPSIS THALIANA, EMBL:AB000798[PUTATIVE] | Kinase, Protein |
| 14107 | 1742 | TRANSPORTER PROTEIN PEPTIDE TRANSPORT PROTEIN - HORDEUM VULGARE, PIR:T04378[PUTATIVE] | Transporter |
| 14108 | 1743 | TRANSPORTER PROTEIN PEPTIDE TRANSPORT PROTEIN - HORDEUM VULGARE, PIR:T04378[PUTATIVE] | Transporter |
| 14109 | 1744 | TRANSPORTER PROTEIN PEPTIDE TRANSPORT PROTEIN - HORDEUM VULGARE, PIR:T04378[PUTATIVE] | Transporter |
| 14110 | 1745 | TRANSPORTER PROTEIN PEPTIDE TRANSPORT PROTEIN - HORDEUM VULGARE, PIR:T04378[PUTATIVE] | Transporter |
| 14111 | 1746 | TRANSPORTER PROTEIN PEPTIDE TRANSPORT PROTEIN - HORDEUM VULGARE, PIR:T04378[PUTATIVE] | Transporter |
| 14118 | 1747 | MAP3K ALPHA 1 PROTEIN KINASE - BRASSICA NAPUS, EMBL:BNA010091[PUTATIVE] | Kinase, Protein |

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| 14125 | 1748 | PROTEIN KINASE - LIKE RECEPTOR-LIKE PROTEIN KINASE RLK3, ARABIDOPSIS THALIANA, EMBL:ATH011674 | Kinase, Protein |
| 14131 | 1749 | PROTEIN KINASE - LIKE RECEPTOR-LIKE PROTEIN KINASE HOMOLOG, ARABIDOPSIS THALIANA, PIR:T45691 | Kinase, Protein |
| 14149 | 1750 | HISTIDYL-TRNA SYNTHETASE | Synthase |
| 14151 | 1751 | PURPLE ACID PHOSPHATASE PRECURSOR -LIKE PROTEIN PURPLE ACID PHOSPHATASE PRECURSOR PAPI, IPOMOEA BATATAS, EMBL:AF200825 | Phosphatase |
| 14153 | 1752 | PROTEIN KINASE - LIKE MEK KINASE ALPHA, DICTYOSTELIUM DISCOIDEUM, EMBL:AF093689 | Kinase, Protein |
| 14155 | 1753 | PROTEIN KINASE -LIKE NPK1-RELATED PROTEIN KINASE 2 ANP2, ARABIDOPSIS THALIANA, EMBL:AB000798 | Kinase, Protein |
| 14156 | 1754 | DEHYDROGENASE -LIKE PROTEIN ALCOHOL DEHYDROGENASE HOMOLOG, RIPENING-RELATED, TOMATO, PIR:S39508 | Dehydrogenases |
| 14163 | 1755 | SERINE/THREONINE-SPECIFIC PROTEIN KINASE (EC 2.7.1.-) LRRPK, ARABIDOPSIS THALIANA, PIR:T08975[PUTATIVE] | Kinase, Protein |
| 14164 | 1756 | PROTEIN (FRAGMENT) SERINE/THREONINE-SPECIFIC RECEPTOR PROTEIN KINASE, ARABIDOPSIS THALIANA, PIR:S71277[PUTATIVE] | Kinase, Protein |
| 14165 | 1757 | PROTEIN (FRAGMENT) SERINE/THREONINE-SPECIFIC RECEPTOR PROTEIN KINASE (EC 2.7.1.-), ARABIDOPSIS THALIANA, PIR:S71277[PUTATIVE] | Kinase, Protein |
| 14166 | 1758 | SERINE/THREONINE-SPECIFIC RECEPTOR PROTEIN KINASE (EC 2.7.1.-), ARABIDOPSIS THALIANA, PIR:S71277[PUTATIVE] | Kinase, Protein |
| 14167 | 1759 | SERINE/THREONINE-SPECIFIC PROTEIN KINASE (EC 2.7.1.-) LRRPK, ARABIDOPSIS THALIANA, PIR:T08975[PUTATIVE] | Kinase, Protein |
| 14168 | 1760 | RECEPTOR PROTEIN KINASE -LIKE RECEPTOR-LIKE PROTEIN KINASE PRECURSOR, MADAGASCAR PERIWINKLE, PIR:T10060 | Kinase, Protein |

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| 14172 | 1761 | RECEPTOR-LIKE PROTEIN KINASE HOMOLOG RECEPTOR-LIKE PROTEIN KINASE - CATHARANTHUS ROSEUS, EMBL:Z73295 | Kinase, Protein |
| 14173 | 1762 | RECEPTOR-LIKE PROTEIN KINASE HOMOLOG LIGHT REPRESSIBLE RECEPTOR PROTEIN KINASE - ARABIDOPSIS THALIANA, PIR:S71277 | Kinase, Protein |
| 14174 | 1763 | RECEPTOR-LIKE PROTEIN KINASE HOMOLOG LIGHT REPRESSIBLE RECEPTOR PROTEIN KINASE - ARABIDOPSIS THALIANA, PIR:S71277 | Kinase, Protein |
| 14176 | 1764 | RECEPTOR-LIKE PROTEIN KINASE HOMOLOG LIGHT REPRESSIBLE RECEPTOR PROTEIN KINASE - ARABIDOPSIS THALIANA, PIR:S71277 | Kinase, Protein |
| 14179 | 1765 | LIGHT REPRESSIBLE RECEPTOR PROTEIN KINASE - ARABIDOPSIS THALIANA, PIR:S71277[PUTATIVE] | Kinase, Protein |
| 14188 | 1766 | GIBBERELLIN 20-OXIDASE, SEVERAL OXIDASES, MAINLY [PUTATIVE] | Oxidase |
| 14189 | 1767 | GIBBERELLIN 20-OXIDASE, SEVERAL OXIDASES, MAINLY [PUTATIVE] | Oxidase |
| 14196 | 1768 | GLUCOSIDASE-LIKE PROTEIN GLUCAN ENDO-1,3- BETA-GLUCOSIDASE PRECURSOR - TRITICUM AESTIVUM, SWISSPROT:E13B_WHEAT | Glycosylase |
| 14204 | 1769 | GLUCOSYLTRANSFERASE-LIKE PROTEIN UDP- GLUCOSE GLUCOSYLTRANSFERASE - ARABIDOPSIS THALIANA, EMBL:AB016819 | Transferases |
| 14205 | 1770 | GLUCOSYLTRANSFERASE-LIKE PROTEIN UDP- GLUCOSE GLUCOSYLTRANSFERASE - ARABIDOPSIS THALIANA, EMBL:AB016819 | Transferases |
| 14206 | 1771 | GLUCOSYLTRANSFERASE-LIKE PROTEIN UDP- GLUCOSE GLUCOSYLTRANSFERASE - ARABIDOPSIS THALIANA, EMBL:AB016819 | Transferases |
| 14207 | 1772 | GLUCOSYLTRANSFERASE-LIKE PROTEIN UDP- GLUCOSE GLUCOSYLTRANSFERASE - ARABIDOPSIS THALIANA, EMBL:AB016819 | Transferases |

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| 14208 | 1773 | GLUCURONOSYL TRANSFERASE-LIKE PROTEIN GLUCURONOSYL TRANSFERASE HOMOLOG, RIPENING-RELATED - LYCOPERSICON ESCULENTUM,PIR2:S39507 | Transferases |
| 14209 | 1774 | GLUCURONOSYL TRANSFERASE-LIKE PROTEIN GLUCURONOSYL TRANSFERASE HOMOLOG, RIPENING-RELATED - LYCOPERSICON ESCULENTUM,PIR2:S39507 | Transferases |
| 14211 | 1775 | GLUCURONOSYL TRANSFERASE-LIKE PROTEIN GLUCURONOSYL TRANSFERASE HOMOLOG, RIPENING-RELATED - LYCOPERSICON ESCULENTUM,PIR2:S39507 | Transferases |
| 14213 | 1776 | CHLOROPLAST IMPORT-ASSOCIATED CHANNEL PROTEIN HOMOLOG CHLOROPLAST IMPORT- ASSOCIATED CHANNEL IAP75 - PISUM SATIVUM,PIR2:S55344 | Channel |
| 14215 | 1777 | RECEPTOR-LIKE PROTEIN KINASE RECEPTOR LIKE PROTEIN KINASE - ARABIDOPSIS THALIANA,PID:E1188577 | Kinase, Protein |
| 14223 | 1778 | SUBTILISIN-LIKE PROTEINASE CUCUMISIN (SERINE PROTEASE,EC 3.4.21.25) PRECURSOR - CUCUMIS MELO,PIR2:A55800 | Protease |
| 14224 | 1779 | SUBTILISIN-LIKE PROTEINASE CUCUMISIN (SERINE PROTEASE,EC 3.4.21.25) PRECURSOR - CUCUMIS MELO,PIR2:A55800 | Protease |
| 14229 | 1780 | COPPER TRANSPORT PROTEIN - LIKE PROTEIN COPPER TRANSPORTER PROTEIN ARABIDOPSIS THALIANA,PID:G1082054 | Transporter |
| 14239 | 1781 | BETA-D-GLUCAN EXOHYDROLASE - LIKE PROTEIN BETA-D-GLUCAN EXOHYDROLASE, NICOTIANA TABACUM, TREMBL:AB017502_1 | Hydrolase |
| 14240 | 1782 | BETA-D-GLUCAN EXOHYDROLASE - LIKE PROTEIN BETA-D-GLUCAN EXOHYDROLASE, NICOTIANA TABACUM, TREMBL:AB017502_1 | Hydrolase |
| 14243 | 1783 | BETA-D-GLUCAN EXOHYDROLASE - LIKE PROTEIN BETA-D-GLUCAN EXOHYDROLASE, NICOTIANA TABACUM, TREMBL:AB017502_1 | Hydrolase |

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| 14244 | 1784 | BETA-D-GLUCAN EXOHYDROLASE - LIKE PROTEIN BETA-D-GLUCAN EXOHYDROLASE, NICOTIANA TABACUM, TREMBL:AB017502_1 | Hydrolase |
| 14248 | 1785 | RECEPTOR KINASE-LIKE PROTEIN RECEPTOR KINASE- LIKE PROTEIN (XA21), ORYZA LONGISTAMINATA, U72725 | Kinase, Protein |
| 14250 | 1786 | RECEPTOR PROTEIN KINASE - LIKE PROTEIN PROTEIN KINASE XA21 RECEPTOR TYPE PRECURSOR, ORYZA SATIVA, PIR:A57676 | Kinase, Protein |
| 14258 | 1787 | 1-AMINOCYCLOPROPANE-1-CARBOXYLIC ACID OXIDASE - LIKE PROTEIN ACC OXIDASE, BRASSICA OLERACEA, X81628 | Oxidase |
| 14274 | 1788 | 11BETA-HYDROXYSTEROID DEHYDROGENASE HOMO SAPIENS,PIR1:DXHUBH[PUTATIVE] | Dehydrogenases |
| 14275 | 1789 | 11BETA-HYDROXYSTEROID DEHYDROGENASE RATTUS NORVEGICUS,PIR1:DXRTBH[PUTATIVE] | Dehydrogenases |
| 14277 | 1790 | PECTINESTERASE HOMOLOG - PINUS RADIATA,PIR2:T08112[PUTATIVE] | Esterase |
| 14279 | 1791 | PECTINESTERASE-LIKE PROTEIN PECTINESTERASE (EC 3.1.1.11) - CITRUS SINENSIS,PID:G2098709 | Esterase |
| 14284 | 1792 | NITRIC OXIDE SYNTHASE, PROTEIN BR-1 PROTEIN HELIX POMATIA,PID:E234055[PUTATIVE] | Synthase |
| 14293 | 1793 | ENDOCHITINASE-LIKE PROTEIN BASIC ENDOCHITINASE CHB4 PRECURSOR - BRASSICA NAPUS, SWISSPROT:CHI4_BRANA | Chitinase |
| 14297 | 1794 | RECEPTOR KINASE-LIKE PROTEIN PROTEIN KINASE XA21 - ORYZA SATIVA, PIR:A57676 | Kinase, Protein |
| 14306 | 1795 | PECTINESTERASE - ARABIDOPSIS THALIANA, PIR:S51370[PUTATIVE] | Esterase |
| 14318 | 1796 | ABC-TYPE TRANSPORT PROTEIN-LIKE PROTEIN ATP BINDING CASSETTE TRANSPORTER ABC2, HOMO SAPIENS ,PIR2:B54774 | Transporter |
| 14334 | 1797 | PEPTIDE TRANSPORTER PEPTIDE TRANSPORTER (PTR1), HORDEUM VULGARE, AF023472[PUTATIVE] | Transporter |

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| 14339 | 1798 | CYCLIC NUCLEOTIDE-GATED CHANNEL CYCLIC NUCLEOTIDE-GATED CATION CHANNEL, ARABIDOPSIS THALIANA, AF067798[PUTATIVE] | Channel |
| 14349 | 1799 | GLYCINE--TRNA LIGASE PRECURSOR, CHLOROPLAST (EDD1) | Ligase |
| 14371 | 1800 | LIPASE - LIKE PROTEIN LIPASE ARAB-1, ARABIDOPSIS THALIANA, PIR2:S68410 | Lipase |
| 14378 | 1801 | DEOXYCYTIDYLATE DEAMINASE - HOMO SAPIENS, PIR:I55434[PUTATIVE] | Deaminase |
| 14382 | 1802 | ENDOXYLOGLUCAN TRANSFERASE-LIKE PROTEIN EXGT1 (ENDOXYLOGLUCAN TRANSFERASE) - PISUM SATIVUM, EMBL:AB015428 | Transferases |
| 14397 | 1803 | GLUTAMATE-1-SEMIALDEHYDE AMINOTRANSFERASE | Transferases |
| 14407 | 1804 | POLY A POLYMERASE, C-TERMINUS POLYADENYLATE-BINDING PROTEINS[PUTATIVE] | Polymerase |
| 14419 | 1805 | ENDO-POLYGALACTURONASE - LIKE PROTEIN ENDO-POLYGALACTURONASE, ARABIDOPSIS THALIANA, GB:CAA05525 | Glycosylase |
| 14424 | 1806 | RNA POLYMERASE III SUBUNIT - LIKE PROTEIN RNA POLYMERASE III SUBUNIT, HOMO SAPIENS, GB:CAB41919 | Polymerase |
| 14435 | 1807 | PEROXIDASE | Oxidase |
| 14436 | 1808 | PEROXIDASE | Oxidase |
| 14440 | 1809 | PYRUVATE KINASE -LIKE PROTEIN VARIOUS PYRUVATE KINASES FROM PROCARYOTES | Kinase |
| 14446 | 1810 | PECTINESTERASE - LIKE PROTEIN PECTINESTERASE, CITRUS SINENSIS, GB:AAB57670 | Esterase |
| 14455 | 1811 | SUGAR TRANSPORTER 2, DROSOPHILA MELANOGASTER, EMBL:AF199484[PUTATIVE] | Transporter |
| 14460 | 1812 | 6-PHOSPHOGLUCONOLACTONASE - LIKE PROTEIN 6-PHOSPHOGLUCONOLACTONASE (6PGL), HOMO SAPIENS, EMBL:HSA243972 | LACTONASE |
| 14491 | 1813 | RECEPTOR PROTEIN KINASE - LIKE PROTEIN CLAVATA1 RECEPTOR KINASE, ARABIDOPSIS THALIANA, EMBL:ATU96879 | Kinase, Protein |
| 14520 | 1814 | PEROXIDASE ATP21A | Oxidase |

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| 14545 | 1815 | FLAVONOL SYNTHASE - LIKE PROTEIN SRG1 PROTEIN, ARABIDOPSIS THALIANA, PIR:S44261 | Synthase |
| 14547 | 1816 | RECEPTOR PROTEIN KINASE -LIKE PROTEIN RECEPTOR-LIKE PROTEIN KINASE (RKL1), ARABIDOPSIS THALIANA, EMBL:AF084034 | Kinase, Protein |
| 14551 | 1817 | ANTHRANILATE HYDROXYCINNAMOYL/BENZOYLTRANSFERASE LIKE PROTEIN ANTHRANILATE HYDROXYCINNAMOYL/BENZOYLTRANSFERASE, DIANTHUS CARYOPHYLLUS | N-Transferases |
| 14552 | 1818 | ANTHRANILATE HYDROXYCINNAMOYL/BENZOYLTRANSFERASE LIKE PROTEIN ANTHRANILATE HYDROXYCINNAMOYL/BENZOYLTRANSFERASE, DIANTHUS CARYOPHYLLUS, PIR:T10717 | N-Transferases |
| 14553 | 1819 | ANTHRANILATE HYDROXYCINNAMOYL/BENZOYLTRANSFERASE, DIANTHUS CARYOPHYLLUS, PIR:T10711[PUTATIVE] | N-Transferases |
| 14554 | 1820 | ANTHRANILATE HYDROXYCINNAMOYL/BENZOYLTRANSFERASE LIKE PROTEIN ANTHRANILATE HYDROXYCINNAMOYL/BENZOYLTRANSFERASE, DIANTHUS CARYOPHYLLUS, PIR:T10719 | N-Transferases |
| 14563 | 1821 | MYOSIN HEAVY CHAIN KINASE B, DICTYOSTELIUM DISCOIDEUM, GB:U90946[PUTATIVE] | Kinase, Protein |
| 14573 | 1822 | REVERSE TRANSCRIPTASE FRAGMENTS[PUTATIVE] | Transcriptase |
| 14576 | 1823 | PHOSPHOGLYCERATE MUTASES[PUTATIVE] | Mutase |
| 14580 | 1824 | STEROID DEHYDROGENASE HOMOLOG - HOMO SAPIENS, EMBL:AF078850[PUTATIVE] | Dehydrogenase |
| 14598 | 1825 | UTP-GLUCOSE GLUCOSYLTRANSFERASE - LIKE PROTEIN UTP-GLUCOSE GLUCOSYLTRANSFERASE, MANIHOT ESCULENTA, PIR:S41951 | Transferases |
| 14600 | 1826 | UDP-GLUCOSE:(GLUCOSYL) LPS ALPHA1,3- GLUCOSYLTRANSFERASE WAAO, E.COLI, EMBL:AF019746[PUTATIVE] | Transferases |

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| 14623 | 1827 | PEROXIDASE-LIKE PROTEIN PEROXIDASE ATP6A - ARABIDOPSIS THALIANA, EMBL:X98774 | Oxidase |
| 14645 | 1828 | STEROID SULFOTRANSFERASE 2 - BRASSICA NAPUS, EMBL:AF000306[PUTATIVE] | Transferases |
| 14648 | 1829 | FLAVANONE 3-HYDROXYLASE (FH3) | Hydroxylase |
| 14661 | 1830 | PROTEIN PHOSPHATASE 2C -LIKE PROTEIN PROTEIN PHOSPHATASE 2C HOMOLOG, MESEMBRYANTHEMUM CRYSTALLINUM, EMBL:AF097667 | Phosphatase |
| 14671 | 1831 | PROTEIN PHOSPHATASE 2C-LIKE PROTEIN PROTEIN PHOSPHATASE-2C, MESEMBRYANTHEMUM CRYSTALLINUM, EMBL:AF075580 | Phosphatase |
| 14672 | 1832 | GLUTAMATE RECEPTOR PUTATIVE GLUTAMATE RECEPTOR GLR2, ARABIDOPSIS THALIANA, EMBL:AF079999[PUTATIVE] | Receptor |
| 14673 | 1833 | SUGAR TRANSPORTER-LIKE PROTEIN SUGAR TRANSPORTER, ARABIDOPSIS THALIANA, EMBL:Z50752 | Transporter |
| 14679 | 1834 | RECEPTOR-PROTEIN KINASE-LIKE PROTEIN RECEPTOR-LIKE PROTEIN KINASE, CATHARANTHUS ROSEUS, PIR:T10060 | Kinase, Protein |
| 14692 | 1835 | SHORT-CHAIN ALCOHOL DEHYDROGENASE-LIKE PROTEIN SHORT-CHAIN ALCOHOL DEHYDROGENASE - ZEA MAYS,PIR:A47542 | Dehydrogenase |
| 14695 | 1836 | PROTEIN KINASE PK1, RECEPTOR-LIKE - ZEA MAYS, PIR:S33532[PUTATIVE] | Kinase, Protein |
| 14706 | 1837 | CHLOROPHYLL SYNTHETASE | Synthase |
| 14710 | 1838 | CA ²⁺ /H ⁺ -EXCHANGING PROTEIN-LIKE ARABIDOPSIS THALIANA HIGH AFFINITY CALCIUM ANTIporter CAX1 ENCODED BY GENBANK ACCESSION NUMBER U57411 | Transporter |
| 14717 | 1839 | MYOSIN HEAVY CHAIN KINASE B - DICTYOSTELIUM DISCOIDEUM, PID:G1903458[PUTATIVE] | Kinase, Protein |
| 14721 | 1840 | WAX SYNTHASE-LIKE PROTEIN WAX SYNTHASE - SIMMONDSIA CHINENSIS, PID:G5020219 | Synthase |
| 14729 | 1841 | DNA POLYMERASE I -BACILLUS STEAROTHERMOPHILUS,PIR2:S70368[PUTATIVE] | Polymerase |

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| 14740 | 1842 | BETA-KETOACYL-COA SYNTHASE LIKE PROTEIN BETA-KETOACYL-COA SYNTHASE - SIMMONDSIA CHINENSIS, PID:G1045614 | Synthase |
| 14750 | 1843 | PSEUDOURIDINE SYNTHASE, PUTATIVE SIMILAR TO RIBOSOMAL LARGE SUBUNIT PSEUDOURIDINE SYNTHASE D SP:P33643 [ESCHERICHIA COLI] | Synthase |
| 14777 | 1844 | PROTEIN KINASE-LIKE PROTEIN - ARABIDOPSIS THALIANA (F15B8.110), PIR2:T06750[PUTATIVE] | Kinase, Protein |
| 14784 | 1845 | BETA-FRUCTOFURANOSIDASE | Glycosylase |
| 14786 | 1846 | PHOSPHATE ACTYLTRANSFERASE, STAPHYLOCOCCUS AUREUS, EMBL:SAU271496[PUTATIVE] | Transferases |
| 14796 | 1847 | CARBONIC ANHYDRASE (CAH1) | Anhydrase |
| 14802 | 1848 | PURPLE ACID PHOSPHATASE-LIKE PROTEIN PURPLE ACID PHOSPHATASE PRECURSOR, PHASEOLUS VULGARIS, EMBL:PVPAPHOSP | Phosphatase |
| 14809 | 1849 | VACUOLAR SORTING RECEPTOR HOMOLOG/ATELPI and SPOT 3 PROTEIN | Receptor |
| 14812 | 1850 | MONODEHYDROASCORBATE REDUCTASE (NADH) - LIKE PROTEIN MONODEHYDROASCORBATE REDUCTASE (NADH), LYCOPERISON ESCULENTUM, PIR:T06407 | Reductase |
| 14825 | 1851 | PROTEIN KINASE, ARABIDOPSIS THALIANA[PUTATIVE] | Kinase, Protein |
| 14832 | 1852 | BETA-GALACTOSIDASE PRECURSOR. LYCOPERSICON ESCULENTUM, GB:P48980[PUTATIVE] | Glycosylase |
| 14838 | 1853 | CAFFEIC ACID O-METHYLTRANSFERASE - LIKE PROTEIN CAFFEIC ACID O-METHYLTRANSFERASE (HOMT1), POPULUS KITAKAMIENSIS, EMBL:PKHOMT1A | Transferases |
| 14839 | 1854 | GLUCOSYLTRANSFERASE - LIKE PROTEIN GLUCOSYLTRANSFERASE IS10A, SALICYLATE- INDUCED, NICOTIANA TABACUM, PIR:T03745 | Transferases |
| 14840 | 1855 | GLUCOSYLTRANSFERASE - LIKE PROTEIN GLUCOSYLTRANSFERASE ISSA, NICOTIANA TABACUM, PIR:T03747 | Transferases |

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| 14841 | 1856 | NODULIN / GLUTAMATE-AMMONIA LIGASE - LIKE PROTEIN MTN6, MEDICAGO TRUNCATULA, EMBL:MTY18225 | Ligase |
| 14842 | 1857 | NODULIN / GLUTAMATE-AMMONIA LIGASE - LIKE PROTEIN MTN6 - NODULIN 6, MEDICAGO TRUNCATULA, EMBL:MET133118 | Ligase |
| 14843 | 1858 | PECTATE LYASE -LIKE PROTEIN PECTATE LYASE, MUSA ACUMINATA, EMBL:MAPEL | Lyase |
| 14851 | 1859 | CLP ENDOPEPTIDASE ATP-BINDING CHAIN C, CHLAMYDIA PNEUMONIAE, PIR:G72079[PUTATIVE] | Protease |
| 14862 | 1860 | RECEPTOR LECTIN KINASE -LIKE PROTEIN RECEPTOR LECTIN KINASE 3, ARABIDOPSIS THALIANA, GB:U93161 | Kinase, Protein |
| 14869 | 1861 | LYSINE DECARBOXYLASE (ECORLD), EIKENELLA CORRODENS, EMBL:U89166[PUTATIVE] | Decarboxylase |
| 14882 | 1862 | DIAMINOPIMELATE EPIMERASE - LIKE PROTEIN DIAMINOPIMELATE EPIMERASE, PSEUDOMONAS FLUORESCENS, PIR:T10459 | Epimerase |
| 14886 | 1863 | INORGANIC PYROPHOSPHATASE -LIKE PROTEIN INORGANIC PYROPHOSPHATASE, SOLANUM TUBEROSUM, PIR:T07399 | Phosphatase |
| 14896 | 1864 | NA(+)/H(+) ANTIPORTER[PUTATIVE] | Transporter |
| 14905 | 1865 | SERINE/THREONINE-SPECIFIC KINASE LIKE PROTEIN SERINE/THREONINE-SPECIFIC KINASE (EC 2.7.1.-) PRECURSOR - ARABIDOPSIS THALIANA, PIR:S68589 | Kinase, Protein |
| 14908 | 1866 | PROTEIN KINASE-LIKE PROTEIN WALL-ASSOCIATED KINASE 4 - ARABIDOPSIS THALIANA, EMBL:ATH9695 | Kinase, Protein |
| 14914 | 1867 | URACIL PHOSPHORIBOSYLTRANSFERASE-LIKE PROTEIN URACIL PHOSPHORIBOSYLTRANSFERASE - NICOTIANA TABACUM, PIR:T03969 | Transferases |
| 14915 | 1868 | MALAT DEHYDROGENASE [PUTATIVE] | Dehydrogenase |
| 14919 | 1869 | GLYOXAL OXIDASE (GLX2) - PHANEROCHAETE CHRYSPORIUM, EMBL:L47287[PUTATIVE] | Oxidase |
| 14927 | 1870 | PROTEIN KINASE -LIKE PROTEIN PROTEIN KINASE APK1, ARABIDOPSIS THALIANA, PIR:S28615 | Kinase, Protein |

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| 14933 | 1871 | FRUCTOKINASE - LIKE PROTEIN FRUCTOKINASE, LYCOPERSICON ESCULENTUM, EMBL:LEU62329 | Kinase |
| 14948 | 1872 | ESTERASE, PSEUDOMONAS FLUORESCENS, EMBL:PF12537[PUTATIVE], PROTEIN (FRAGMENT) | Esterase |
| 14966 | 1873 | CHITINASE CLASS IV (CHIV) | Chitinase |
| 14969 | 1874 | RNA POLYMERASE 24KDA SUBUNIT -LIKE PROTEIN RNA POLYMERASE SUBUNIT, ARABIDOPSIS THALIANA, EMBL:AF019248 | Polymerase |
| 14985 | 1875 | SUGAR-PHOSPHATE ISOMERASE - LIKE PROTEIN GUTQ/KPSF FAMILY SUGAR-P ISOMERASE, CHLAMYDIA PNEUMONIAE, PIR:E72068 | Isomerase |
| 14986 | 1876 | PHOSPHATE TRANSPORT PROTEIN PHOSPHATE TRANSPORTER, NICOTIANA TABACUM, EMBL:AB020061 | Transporter |
| 14999 | 1877 | VESICULAR TRANSPORTER UNC-47, CAENORHABDITIS ELEGANS, AF031935[PUTATIVE] | Transporter |
| 15008 | 1878 | PECTATE LYASE - LIKE PROTEIN PECTATE LYASE, MUSA ACUMINATA, X92943 | Lyase |
| 15019 | 1879 | PHOSPHATIDYLGLYCEROPHOSPHATE SYNTHASE - LIKE PROTEIN PHOSPHATIDYLGLYCEROPHOSPHATE SYNTHASE, PSEUDOMONAS FLUORESCENS, EMBL:L29642 | Synthase |
| 15021 | 1880 | PROTEIN PHOSPHATASE 2C - LIKE PROTEIN PROTEIN PHOSPHATASE 2C HOMOLOG, MESEMBRYANTHEMUM CRYSTALLINUM, EMBL AF097667 | Phosphatase |
| 15028 | 1881 | CHALCONE ISOMERASE | Isomerase |
| 15034 | 1882 | LIPASE -LIKE PROTEIN MONOGLYCERIDE LIPASE, MUS MUSCULUS, EMBL:MMMGLYLIP | Lipase |
| 15035 | 1883 | LIPASE -LIKE PROTEIN MONOGLYCERIDE LIPASE, MUS MUSCULUS, EMBL:MMMGLYLIP | Lipase |
| 15041 | 1884 | PECTATE-LYASE, ARABIDOPSIS THALIANA, PIR:T06728[PUTATIVE] | Lyase |
| 15043 | 1885 | DUAL SPECIFICITY PROTEIN PHOSPHATASE 5, PHOSPHATASE - LIKE PROTEIN, RATTUS NORWEGICUS, SWISSPROT:DUS5_RAT | Phosphatase |

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| 15045 | 1886 | ALCOHOL DEHYDROGENASE HOMOLOG, TOMATO, PIR:S3950811BETA-HYDROXYSTEROID DEHYDROGENASE (EC 1.1.1.146) I - MOUSE, PIR:I56604[PUTATIVE] OXIDOREDUCTASE -LIKE PROTEIN RIPENING-RELATED | Dehydrogenases |
| 15047 | 1887 | BETA-KETOACYL-ACP REDUCTASE - LIKE PROTEIN BETA-KETOACYL-ACP REDUCTASE, CUPHEA LANCEOLATA, EMBL:X64566 | Reductase |
| 15059 | 1888 | BETA-1,3-GLUCANASE - LIKE PROTEIN PROBABLE BETA-1,3-GLUCANASE, TRITICUM AESTIVUM, PIR:T06268 | Glycosylase |
| 15061 | 1889 | SERINE/THREONINE-SPECIFIC PROTEIN KINASE -LIKE SERINE/THREONINE-SPECIFIC PROTEIN KINASE NAK, ARABIDOPSIS THALIANA, PIR:S38326 | Kinase, Protein |
| 15086 | 1890 | GLUCURONOSYL TRANSFERASE - LIKE PROTEIN GLUCURONOSYL TRANSFERASE HOMOLOG, LYCOPERSICON ESCULENTUM, PIR:S39507 | Transferases |
| 15087 | 1891 | GLUCURONOSYL TRANSFERASE - LIKE PROTEIN GLUCURONOSYL TRANSFERASE HOMOLOG, LYCOPERSICON ESCULENTUM, PIR:S39507 | Transferases |
| 15090 | 1892 | PROLINE TRANSPORTER 2 | Transporter |
| 15094 | 1893 | BETA-1,3-GLUCANASE - LIKE PROTEIN BETA-1,3- GLUCANASE, ARABIDOPSIS THALIANA, PIR:S31906 | Glycosylase |
| 15096 | 1894 | SEDOHEPTULOSE-BISPHOSPHATASE PRECURSOR | Phosphatase |
| 15103 | 1895 | ANTHRANILATE SYNTHASE ALPHA-1 CHAIN - LIKE PROTEIN ANTHRANILATE SYNTHASE ALPHA SUBUNIT, RUTA GRAVEOLENS, EMBL:RGANTSYNB | Synthase |
| 15111 | 1896 | RECEPTOR KINASE - LIKE PROTEIN RECEPTOR KINASE HOMOLOG CRINKLY4, MAIZE, PIR:T04108 | Kinase, Protein |
| 15113 | 1897 | LEUCOANTHOCYANIDIN DIOXYGENASE -LIKE PROTEIN LEUCOANTHOCYANIDIN DIOXYGENASE, APPLE TREE, PIR:S33144 | Oxygenases |
| 15116 | 1898 | CELLULOSE SYNTHASE (CELA), AGROBACTERIUM TUMEFACIENS, EMBL:ATCELABCE[PUTATIVE] | Synthase |

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| 15121 | 1899 | PROTEIN KINASE SERINE/THREONINE-SPECIFIC PROTEIN KINASE NPK15 - NICOTIANA TABACUM, PIR:S52578[PUTATIVE] | Kinase, Protein |
| 15122 | 1900 | MANDELONITRILE LYASE-LIKE PROTEIN ADHESION OF CALYX EDGES (ACE) - ARABIDOPSIS THALIANA | Lyase |
| 15129 | 1901 | ACETYL-COA CARBOXYLASE, BIOTIN CARBOXYL CARRIER - ANABAENA SP., PIR:B53311[PUTATIVE] | Carboxylase |
| 15136 | 1902 | GLUTAMINE TRANSPORTER NEURONAL - RATTUS NORVEGICUS, EMBL:AF075704[PUTATIVE] | Transporter |
| 15144 | 1903 | PROTEIN KINASE NPK1-RELATED PROTEIN KINASE 1S - ARABIDOPSIS THALIANA, EMBL:AB000797 | Kinase, Protein |
| 15148 | 1904 | POLY(A) POLYMERASE - CANDIDA ALBICANS, EMBL:AB009394[PUTATIVE] | Polymerase |
| 15149 | 1905 | N2,N2-DIMETHYLGUANOSINE TRNA METHYLTRANSFERASES-LIKE PROTEIN SEVERAL N2,N2-DIMETHYLGUANOSINE TRNA METHYLTRANSFERASES | Transferases |
| 15153 | 1906 | LEUCINE-RICH RECEPTOR-LIKE PROTEIN KINASE - MALUS DOMESTICA, EMBL:AF053127[PUTATIVE] | Kinase, Protein |
| 15162 | 1907 | QUINONE REDUCTASE-LIKE PROTEIN ZETA- CRYSTALLIN / QUINONE REDUCTASE (NADPH) - MUS MUSCULUS, PIR:A54932 | Reductase |
| 15200 | 1908 | GLYCEROL-3-PHOSPHATE DEHYDROGENASES - BACTERIA[PUTATIVE] | Dehydrogenases |
| 15224 | 1909 | DNA-DIRECTED RNA POLYMERASE II 23 KD POLYPEPTIDE (RPB25) - HOMO SAPIENS, EMBL:J04965[PUTATIVE] | Polymerase |
| 15240 | 1910 | BETA-1,3-GLUCANASE | Glycosylase |
| 15242 | 1911 | BETA-1,3-GLUCANASE 2 (BG2) (PR-2) | Glycosylase |
| 15243 | 1912 | GLUCAN ENDO-1,3-BETA-D-GLUCOSIDASE-LIKE PROTEIN GLUCAN ENDO-1,3-BETA-D-GLUCOSIDASE - GLYCINE MAX, PIR:T07108 | Glycosylase |
| 15263 | 1913 | METALLOENDOPEPTIDASE NRD2 CONVERTASE - RATTUS SP, EMBL: X93208[PUTATIVE] | Protease |
| 15264 | 1914 | PROTEASE-LIKE PROTEIN INSULIN-DEGRADING ENZYME - RATTUS NORVEGICUS, SWISSPROT:P35559 | Protease |

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| 15268 | 1915 | ENDO-POLYGALACTURONASE | Glycosylase |
| 15273 | 1916 | ACETYLGLUTAMATE KINASE-LIKE PROTEIN ACETYLGLUTAMATE KINASE - SYNECHOCYSTIS SP., PIR:S77509 | Kinase |
| 15279 | 1917 | GALACTOSE OXIDASE PRECURSO, CLADOBOTRYUM DENDROIDES, PIR2:A38084[PUTATIVE] | Oxidase |
| 15281 | 1918 | WALL-ASSOCIATED KINASE 1, ARABIDOPSIS THALIANA, AJ009696[PUTATIVE] | Kinase, Protein |
| 15283 | 1919 | DNA-DIRECTED RNA POLYMERASE I 190K CHAIN - LIKE PROTEIN DNA-DIRECTED RNA POLYMERASE(EC 2.7.7.6) I 190K CHAIN, SACCHAROMYCES CEREVISIAE, PIR2:S67250 | Polymerase |
| 15285 | 1920 | CARBOXYL TERMINAL PROTEASE - LIKE PROTEIN CARBOXYL TERMINAL PROTEASE, NOSTOC PUNCTIFORME, AF022823 | Protease |
| 15287 | 1921 | WALL-ASSOCIATED KINASE 4, ARABIDOPSIS THALIANA, AJ009695 | Kinase, Protein |
| 15288 | 1922 | WALL-ASSOCIATED KINASE 4, ARABIDOPSIS THALIANA, AJ009695 | Kinase, Protein |
| 15289 | 1923 | PROTEIN KINASE - LIKE PROTEIN S-RECEPTOR KINASE (EC 2.7.1.-) PRECURSOR, BRASSICA OLERACEA, PIR1:S31429 | Kinase, Protein |
| 15290 | 1924 | WALL-ASSOCIATED KINASE 1, ARABIDOPSIS THALIANA, AJ009696[PUTATIVE] | Kinase, Protein |
| 15291 | 1925 | WALL-ASSOCIATED KINASE 4, ARABIDOPSIS THALIANA, AJ009695[PUTATIVE] | Kinase, Protein |
| 15292 | 1926 | WALL-ASSOCIATED KINASE 1, ARABIDOPSIS THALIANA, AJ009696 | Kinase, Protein |
| 15293 | 1927 | WALL-ASSOCIATED KINASE 1, ARABIDOPSIS THALIANA, AJ009696[PUTATIVE] | Kinase, Protein |
| 15294 | 1928 | WALL-ASSOCIATED KINASE 4, ARABIDOPSIS THALIANA, AJ009695 | Kinase, Protein |
| 15296 | 1929 | POLYGALACTURONASE (EC 3.2.1.15) PRECURSOR, ERWINIA CAROTOVORA, PIR:S11773[PUTATIVE] | Glycosylase |
| 15300 | 1930 | RECEPTOR-LIKE PROTEIN KINASE SEVERAL RECEPTOR-LIKE PROTEIN KINASES | Kinase, Protein |

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| 15305 | 1931 | ANTHRANILATE PHOSPHORIBOSYLTRANSFERASE- LIKE PROTEIN ANTHRANILATE PHOSPHORIBOSYLTRANSFERASE - PISUM SATIVUM, PIR:T06460 | Transferases |
| 15327 | 1932 | GLUCAN ENDO-1,3-BETA-GLUCOSIDASE PRECURSOR - TRITICUM AESTIVUM, SWISSPROT:P52409[PUTATIVE] | Glycosylase |
| 15366 | 1933 | SPHINGOLIPID TRANSPORT PROTEIN LCB3 - SACCHAROMYCES CEREVISIAE, PIR:S55178[PUTATIVE] | Transporter |
| 15378 | 1934 | KETOL-ACID REDUCTOISOMERASE | Isomerase |
| 15386 | 1935 | SERINE/THREONINE-SPECIFIC PROTEIN KINASE -LIKE PROTEIN SERINE/THREONINE-SPECIFIC PROTEIN KINASE NAK, ARABIDOPSIS THALIANA, PIR:S38326 | Kinase, Protein |
| 15391 | 1936 | CITRATE SYNTHASE -LIKE PROTEIN CITRATE SYNTHASE, CUCURBIT, PIR:S53007 | Synthase |
| 15392 | 1937 | CITRATE SYNTHASE -LIKE PROTEIN CITRATE SYNTHASE, CUCURBIT, PIR:S53007 | Synthase |
| 15393 | 1938 | TYROSINE KINASE, DICTYOSTELIUM DISCOIDEUM, PIR:A35670[PUTATIVE] | Kinase, Protein |
| 15399 | 1939 | RIBOSOMAL RNA APURINIC SITE SPECIFIC LYASE, TRITICUM AESTIVUM, EMBL:AB032123[PUTATIVE] | Lyase |
| 15416 | 1940 | 3-ISOPROPYLMALATE DEHYDRATASE-LIKE PROTEIN (SMALL SUBUNIT) 3-ISOPROPYLMALATE DEHYDRATASE, SMALL SUBUNIT - THERMOTOGA MARITIMA, PIR:A72363 | Dehydratase |
| 15418 | 1941 | PECTINESTERASE PRECURSOR-LIKE PROTEIN PECTINESTERASE (EC 3.1.1.11) PRECURSOR - PISUM SATIVUM, PIR:T06468 | Esterase |
| 15427 | 1942 | CALLOSE SYNTHASE CATALYTIC SUBUNIT (CFL1) - GOSSYPIUM HIRSUTUM, EMBL:AF085717[PUTATIVE] | Synthase |
| 15428 | 1943 | RECEPTOR-LIKE PROTEIN KINASE RECEPTOR-LIKE PROTEIN KINASE (RKS2) - ARABIDOPSIS THALIANA, EMBL:AF084036 | Kinase, Protein |
| 15431 | 1944 | ABC TRANSPORTER-LIKE PROTEIN PUTATIVE MULTI RESISTANCE PROTEIN MRP - ARABIDOPSIS THALIANA, EMBL:ATMRPPROT | Transporter |

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| 15452 | 1945 | PROTEIN KINASE-LIKE PROTEIN PTO KINASE INTERACTOR 1 - LYCOPERSICON ESCULENTUM, EMBL:U28007 | Kinase, Protein |
| 15453 | 1946 | TRANSPORTER-LIKE PROTEIN UDP-GALACTOSE TRANSPORT PROTEIN HOMOLOG - SCHIZOSACCHAROMYCES POMBE, PIR:T43506 | Transporter |
| 15459 | 1947 | RECEPTOR KINASE HOMOLOG CRINKLY4 - ZEA MAYS, PIR:T04108[PUTATIVE] | Kinase, Protein |
| 15465 | 1948 | FRUCTOKINASE-LIKE PROTEIN FRUCTOKINASE - LYCOPERSICON ESCULENTUM, EMBL:LEU62329 | Kinase |
| 15487 | 1949 | SERINE/THREONINE-SPECIFIC KINASE LECRK1 PRECURSOR, LECTIN RECEPTOR-LIKE | Kinase, Protein |
| 15490 | 1950 | RECEPTOR LECTIN KINASE-LIKE PROTEIN (FRAGMENT) RECEPTOR LECTIN KINASE 3 - ARABIDOPSIS THALIANA, EMBL:U93161 | Kinase, Protein |
| 15491 | 1951 | RECEPTOR LECTIN KINASE 3 | Kinase, Protein |
| 15492 | 1952 | RECEPTOR LECTIN KINASE-LIKE PROTEIN RECEPTOR LECTIN KINASE 3 - ARABIDOPSIS THALIANA, EMBL:U93161 | Kinase, Protein |
| 15500 | 1953 | SERINE/THREONINE-PROTEIN KINASE CTR1 - ARABIDOPSIS THALIANA, EMBL:L08789[PUTATIVE] | Kinase, Protein |
| 15502 | 1954 | POLYGALACTURONASE-LIKE PROTEIN POLYGALACTURONASE - PRUNUS PERSICA, PIR:S40123 | Glycosylase |
| 15506 | 1955 | DIHYDRODIPICOLINATE REDUCTASES (DAPB)[PUTATIVE] | Reductase |
| 15579 | 1956 | PHOSPHATIDATE CYTIDYLYLTRANSFERASE - LIKE PROTEIN PHOSPHATIDATE CYTIDYLYLTRANSFERASE, SYNECHOCYSTIS SP., PIR:S77254 | Transferases |
| 15590 | 1957 | PECTINESTERASE - LIKE PROTEIN PECTINESTERASE, SWEET ORANGE, PIR:T10494 | Esterase |
| 15605 | 1958 | DIHYDRODIPICOLINATE SYNTHASE PRECURSOR | Synthase |
| 15612 | 1959 | APURINIC ENDONUCLEASE - ARABIDOPSIS THALIANA, EMBL:X76912 (AT C-TERMINUS)[PUTATIVE] | Nuclease |
| 15620 | 1960 | APURINIC ENDONUCLEASE - ARABIDOPSIS THALIANA, EMBL:X76912 (AT C-TERMINUS)[PUTATIVE] | Nuclease |

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| 15647 | 1961 | ANTHRANILATE PHOSPHORIBOSYLTRANSFERASE- LIKE PROTEIN ANTHRANILATE PHOSPHORIBOSYLTRANSFERASE (FRAGMENT) - PISUM SATIVUM, PIR:T06460 | Transferases |
| 15657 | 1962 | 1-AMINOCYCLOPROPANE-1-CARBOXYLATE OXIDASE- LIKE PROTEIN 1-AMINOCYCLOPROPANE-1- CARBOXYLATE OXIDASE HOMOLOG - ARABIDOPSIS THALIANA, PIR:S59548 | Oxidase |
| 15658 | 1963 | PROTEIN KINASE HOMOLOG F4118.11 - ARABIDOPSIS THALIANA, PIR:T02456[PUTATIVE] | Kinase, Protein |
| 15666 | 1964 | POLYGALACTURONASE - ZEA MAYS, EMBL:ZMPGAL3[PUTATIVE] | Glycosylase |
| 15670 | 1965 | 3-METHYL-2-OXOBUTANOATE HYDROXY-METHYL- TRANSFERASE-LIKE PROTEIN KETOPANTOATE HYDROXYMETHYLTRANSFERASE - EMERICELLA NIDULANS, EMBL:AF134703 | Transferases |
| 15671 | 1966 | PROLYL AMINOPEPTIDASE-LIKE PROTEIN PROLYL AMINOPEPTIDASE - AEROMONAS SOBRIA, PIR:JC4184 | Protease |
| 15689 | 1967 | ANTHRANILATE PHOSPHORIBOSYLTRANSFERASE - PISUM SATIVUM, EMBL:D86180[PUTATIVE] | Transferases |
| 15698 | 1968 | BETA-1,3-GLUCANASE PRECURSOR - ORYZA SATIVA, EMBL:U72255[PUTATIVE] | Glycosylase |
| 15716 | 1969 | O-METHYLTRANSFERASE - DIFFERENT SPECIES[PUTATIVE] | Transferases |
| 15723 | 1970 | PECTINACETYLESTERASE PRECURSOR-LIKE PROTEIN PECTINACETYLESTERASE PRECURSOR - VIGNA RADIATA, EMBL:X99348 | Esterase |
| 15728 | 1971 | POLYGALACTURONASE - LYCOPERSICON ESCULENTUM, EMBL:AF118567[PUTATIVE] | Glycosylase |
| 15730 | 1972 | ISOPENICILLIN N EPIMERASE - STREPTOMYCES CLAVULIGERUS, EMBL:M32324[PUTATIVE] | Epimerase |
| 15733 | 1973 | 10-DEACETYLBACCATIN III-10-O-ACETYL TRANSFERASE - TAXUS CUSPIDATA, EMBL:AF193765[PUTATIVE] | Transferases |
| 15734 | 1974 | PECTINESTERASE-LIKE PROTEIN PECTINESTERASE - BRASSICA RAPA, EMBL:L48178 | Esterase |

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| 15735 | 1975 | PECTIN METHYLESTERASE - ARABIDOPSIS THALIANA, EMBL:AJ250430[PUTATIVE] | Esterase |
| 15768 | 1976 | protein DISULFIDE-ISOMERASE - ZEA MAYS, PIR:S69181[PUTATIVE] | Isomerase |
| 15782 | 1977 | MITOCHONDRIAL CARRIER PROTEIN AT2G47490 - ARABIDOPSIS THALIANA, EMBL:AC002535[PUTATIVE] | Transporter |
| 15783 | 1978 | GLYCOSYL TRANSFERASE LGTC - NEISSERIA GONORRHOEA, EMBL:AF208062[PUTATIVE] | Transferases |
| 15787 | 1979 | ABC TRANSPORTER-LIKE PROTEIN GLUTATHIONE-CONJUGATE TRANSPORTER ATMRP4 - ARABIDOPSIS THALIANA, EMBL:AJ002584 | Transporter |
| 15788 | 1980 | BETA-D-GLUCAN EXOHYDROLASE-LIKE PROTEIN EXHYDROLASE II - ZEA MAYS, EMBL:AF064707 | Hydrolase |
| 15789 | 1981 | ALPHA GALACTOSYLTRANSFERASE-LIKE PROTEIN ALPHA GALACTOSYLTRANSFERASE - TRIGONELLA FOENUM-GRAECUM, EMBL:TFO245478 | Transferases |
| 15793 | 1982 | GLUTATHIONE TRANSFERASE III-LIKE PROTEIN GLUTATHIONE TRANSFERASE III(B) - ZEA MAYS, EMBL:AJ010296 | Transferases |
| 15799 | 1983 | PECTINESTERASE HOMOLOG - PINUS RADIATA, PIR:T08112[PUTATIVE] | Esterase |
| 15803 | 1984 | LYSOPHOSPHOLIPASE HOMOLOG - ORYZA SATIVA, PIR:T02661[PUTATIVE] | Lipase |
| 15805 | 1985 | AMINO ACID SELECTIVE CHANNEL PROTEIN HORDEUM VULGARE, EMBL:AJ011921[PUTATIVE] | Channel |
| 15828 | 1986 | TRNA ISOPENTENYL TRANSFERASE -LIKE PROTEIN TRNA ISOPENTENYL TRANSFERASE, ARABIDOPSIS THALIANA, EMBL:AF109376 | Transferases |
| 15845 | 1987 | SERINE/THREONINE-PROTEIN KINASE NEK4 - MUS MUSCULUS, EMBL:AF099067[PUTATIVE] | Kinase, Protein |
| 15849 | 1988 | PROTEIN PHOSPHATASE 2C - RATTUS NORVEGICUS, EMBL:AF095927[PUTATIVE] | Phosphatase |
| 15850 | 1989 | MAP KINASE [PUTATIVE] | Kinase, Protein |
| 15851 | 1990 | PROTEIN PHOSPHATASE 2C - RATTUS NORVEGICUS, EMBL:AF095927[PUTATIVE] | Phosphatase |

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| 15861 | 1991 | CYTOKININ OXIDASE -LIKE PROTEIN CYTOKININ OXIDASE, ZEA MAYS, EMBL:ZMY18377 | Oxidase |
| 15873 | 1992 | CHALCONE SYNTHASE SIMILAR TO PLANT CHALCONE AND STILBENE SYNTHASES[PUTATIVE] | Synthase |
| 15880 | 1993 | NUCLEOTIDE SUGAR EPIMERASE [PUTATIVE] | Epimerase |
| 15888 | 1994 | PECTINESTERASE [PUTATIVE] | Esterase |
| 15892 | 1995 | CUCUMISIN PROTEASE [PUTATIVE] | Protease |
| 15893 | 1996 | PHOSPHOLIPASE D-LIKE PROTEIN | Lipase |
| 15897 | 1997 | LIGHT REPRESSIBLE RECEPTOR PROTEIN KINASE (PID:E242366), SIMILAR TO A. THALIANA | Kinase, Protein |
| 15903 | 1998 | S-DOMAIN RECEPTOR-LIKE PROTEIN KINASE, ZEA MAYS, SIMILARITY TO | Kinase, Protein |
| 15918 | 1999 | BETA-AMYLASE SIMILAR TO THE FAMILY OF GLYCOSYL HYDROLASES[PUTATIVE] | Hydrolase |
| 15921 | 2000 | ACETYL COA THIOESTERASE [PUTATIVE] | Esterase |
| 15925 | 2001 | DTDP-6-DEOXY-L-MANNOSE-DEHYDROGENASE [PUTATIVE] | Dehydrogenases |
| 15932 | 2002 | POTASSIUM/H+ ANTIPTORTER [PUTATIVE] | Transporter |
| 15939 | 2003 | PHOSPHORIBOSYLANTHRANILATE TRANSFERASE [PUTATIVE] | Transferases |
| 15970 | 2004 | CYCLIC NUCLEOTIDE GATED CHANNEL (CNGC4) LIKE PROTEIN ARABIDOPSIS THALIANA CYCLIC NUCLEOTIDE GATED CHANNEL (CNGC4),PID:G4378659 | Channel |
| 15976 | 2005 | FLAVONOL GLUCOSYLTRANSFERASE SIMILAR TO MANIHOT ESCULENTA FLAVONOL 3-O-GLUCOSYLTRANSFERASE 5, GENBANK ACCESSION NUMBER Q40287[PUTATIVE] | Transferases |
| 15982 | 2006 | ACETYLTRANSFERASE SIMILAR TO DIGITALIS LANATA LANATOSIDE 15'-O-ACETYLTRANSFERASE, GENBANK ACCESSION NUMBER AJ011567[PUTATIVE] | Transferases |
| 16002 | 2007 | PROTEIN KINASE [PUTATIVE] | Kinase, Protein |
| 16011 | 2008 | CALCIUM-REGULATED PROTEIN PHOSPHATASE SIMILAR TO N. CRASSA CALCINEURIN CALCIUM-REGULATED PROTEIN PHOSPHATASE, GENBANK ACCESSION NUMBER P87072[PUTATIVE] | Phosphatase |
| 16016 | 2009 | WATER CHANNEL PROTEIN [PUTATIVE] | Channel |

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| 16017 | 2010 | INORGANIC PHOSPHATASE [PUTATIVE] | Phosphatase |
| 16022 | 2011 | REVERSE TRANSCRIPTASE-LIKE PROTEIN [PUTATIVE] | Transcriptase |
| 16037 | 2012 | PROTOPORPHYRINOGEN OXIDASE | Oxidase |
| 16038 | 2013 | CHITINASE SIMILAR TO PEANUT TYPE II CHITINASE, GENBANK ACCESSION NUMBER X82329, E.C. 3.2.1.14[PUTATIVE] | Chitinase |
| 16048 | 2014 | SECA-TYPE CHLOROPLAST PROTEIN TRANSPORT FACTOR [PUTATIVE] | Transporter |
| 16049 | 2015 | PROTEIN TRANSPORT FACTOR [PUTATIVE] | Transporter |
| 16052 | 2016 | POTASSIUM CHANNEL [PUTATIVE] | Channel |
| 16065 | 2017 | RAFFINOSE SYNTHASE OR SEED IMBIBITION PROTEIN SIMILAR TO CUCUMBER RAFFINOSE SYNTHASE, GENBANK ACCESSION NUMBER AF073744[PUTATIVE] | Synthase |
| 16069 | 2018 | NAK-LIKE SER/THR PROTEIN KINASE SIMILAR TO A. THALIANA NAK SER/THR PROTEIN KINASE, GENBANK ACCESSION NUMBER P43293[PUTATIVE] | Kinase, Protein |
| 16081 | 2019 | GLYCOSYL TRANSFERASE SIMILAR TO LGTC OF NEISSERIA SP., GENBANK ACCESSION NUMBER U14554, SIMILAR TO LGTC, GENBANK ACCESSION NUMBER U65788 | Transferases |
| 16094 | 2020 | GTP PYROPHOSPHOKINASE SIMILAR TO BACTERIAL GTP PYROPHOSPHOKINASES (RELA) SIMILAR TO B. SUBTILIS RELA (EC 2.7.6.5), GENBANK ACCESSION NUMBER 2635224 CARBOXYL REGION OF PROTEIN NOT DEFINED[PUTATIVE] | Kinase |
| 16096 | 2021 | SUCROSE SYNTHETASE SIMILAR TO SEVERAL PLANT SUGAR SYNTHETASES SIMILAR TO P. SATIVUM SECOND SUGAR SYNTHETASE, GENBANK ACCESSION NUMBER AJ001071 SIMILAR TO BEET SUCROSE SYNTHETASE (EC 2.4.1.13), GENBANK ACCESSION NUMBER S71494[PUTATIVE] | Synthase |
| 16098 | 2022 | PECTINESTERASE SIMILAR TO SEVERAL PLANT PECTINESTERASES[PUTATIVE] | Esterase |
| 16100 | 2023 | PECTINESTERASE - LIKE PROTEIN SIMILAR TO BACTERIAL AND FUNGI PECTINESTERASES | Esterase |

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| 16101 | 2024 | PECTINESTERASE, SIMILAR TO | Esterase |
| 16118 | 2025 | GLYCOSYLTRANSFERASE SIMILAR TO A. THALIANA PROTEIN T20K9.11, GENBANK ACCESSION NUMBER 3445207[PUTATIVE] | Transferases |
| 16120 | 2026 | GLUTATHIONE S TRANSFERASE, ATPM24.1 | Transferases |
| 16129 | 2027 | TRYPTOPHAN SYNTHASE ALPHA 1-LIKE PROTEIN SIMILAR TO A. THALIANA TRYPTOPHAN SYNTHASE ALPHA CHAIN (EC 4.2.1.20), GENBANK ACCESSION NUMBER U18993 | Synthase |
| 16131 | 2028 | SERINE/THREONINE PROTEIN KINASE [PUTATIVE] | Kinase, Protein |
| 16137 | 2029 | Glutamate N-METHYL-D-ASPARTATE RECEPTOR; GLUTAMATE-/ASPARTATE-BINDING PEPTIDE SIMILAR TO RAT N-METHYL-D-ASPARTATE RECEPTOR GLUTAMATE-BINDING CHAIN, GENBANK ACCESSION NUMBER S19586[PUTATIVE] | Receptor |
| 16146 | 2030 | ENT-KAURENE SYNTHETASE A - LIKE PROTEIN | Synthase |
| 16173 | 2031 | OXIDOREDUCTASE SIMILAR TO A. THALIANA PUTATIVE PROTEIN F21P8.230, GENBANK ACCESSION NUMBER 3445238[PUTATIVE] | Reductase |
| 16174 | 2032 | GIBBERELLIN 20-OXIDASE, GENBANK ACCESSION NUMBER U70530[PUTATIVE], OXIDOREDUCTASE SIMILAR TO P. VULGARIS | Oxidase |
| 16175 | 2033 | OXIDOREDUCTASE [PUTATIVE] | Reductase |
| 16182 | 2034 | ALCOHOL DEHYDROGENASE SIMILAR TO PLANT SHORT CHAIN ALCOHOL DEHYDROGENASE[PUTATIVE] | Dehydrogenases |
| 16189 | 2035 | XYLOGLUCAN ENDOTRANSGLYCOSYLASE [PUTATIVE] | Glycosylase |
| 16191 | 2036 | RECEPTOR KINASE [PUTATIVE] | Kinase, Protein |
| 16194 | 2037 | PROTEIN PHOSPHATASE REGULATORY SUBUNIT [PUTATIVE] | Phosphatase |
| 16202 | 2038 | GLYCOSYLATION ENZYME SIMILAR TO B. TAURUS CORE2-GLCNAC-TRANSFERASE, GENBANK ACCESSION NUMBER U41320[PUTATIVE] | Transferases |

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| 16207 | 2039 | LRR RECEPTOR-LIKE PROTEIN KINASE SIMILAR TO Z. MAYS LEUCINE-RICH REPEAT TRANSMEMBRANE PROTEIN KINASE LRRTPK 1, GENBANK ACCESSION NUMBER AF023164[PUTATIVE] | Kinase, Protein |
| 16221 | 2040 | REVERSE TRANSCRIPTASE [PUTATIVE] | Transcriptase |
| 16223 | 2041 | GLUCAN SYNTHASE COMPONENT SIMILAR TO 1,3-BETA GLUCAN SYNTHASE[PUTATIVE] | Synthase |
| 16229 | 2042 | HYDROLASE [PUTATIVE] | Hydrolase |
| 16261 | 2043 | PECTINESTERASE [PUTATIVE] | Esterase |
| 16268 | 2044 | REVERSE TRANSCRIPTASE [PUTATIVE] | Transcriptase |
| 16272 | 2045 | PHOSPHOFRUCTOKINASE BETA SUBUNIT [PUTATIVE] | Kinase |
| 16280 | 2046 | REVERSE TRANSCRIPTASE [PUTATIVE] | Transcriptase |
| 16290 | 2047 | DISEASE RESISTANCE PROTEIN SIMILAR TO RECEPTOR PROTEIN KINASES[PUTATIVE] | Kinase, Protein |
| 16317 | 2048 | RECEPTOR-LIKE PROTEIN KINASE [PUTATIVE] | Kinase, Protein |
| 16318 | 2049 | RECEPTOR-LIKE PROTEIN KINASE [PUTATIVE] | Kinase, Protein |
| 16319 | 2050 | RECEPTOR-LIKE PROTEIN KINASE [PUTATIVE] | Kinase, Protein |
| 16322 | 2051 | RECEPTOR-LIKE PROTEIN KINASE [PUTATIVE] | Kinase, Protein |
| 16325 | 2052 | RECEPTOR-LIKE PROTEIN KINASE | Kinase, Protein |
| 16329 | 2053 | 5-ADENYLYLSULFATE REDUCTASE | Reductase |
| 16345 | 2054 | ABC TRANSPORTER SIMILAR TO GUILLARDIA THETA ABC TRANSPORTER, GENBANK ACCESSION NUMBER AF041468[PUTATIVE] | Transporter |
| 16353 | 2055 | POTASSIUM TRANSPORTER SIMILAR TO A. THALIANA K ⁺ ANTIporter KEA1, GENBANK ACCESSION NUMBER AF003382[PUTATIVE] | Transporter |
| 16355 | 2056 | PHOSPHATIDYLGLYCEROTRANSFERASE SIMILAR TO CDP-DIACYLGLYCEROL-GLYCEROL-3-PHOSPHATE 3-PHOSPHATIDYLTRANSFERASE OF SYNECHOCYSTIS SP. GENBANK ACCESSION NUMBER D90914[PUTATIVE] | Transferases |
| 16379 | 2057 | EQUILIBRATIVE NUCLEOSIDE TRANSPORTER 1, HOMO SAPIENS, GB:NP_004946[PUTATIVE] | Transporter |

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| 16380 | 2058 | EQUILIBRATIVE NUCLEOSIDE TRANSPORTER 1, HOMO SAPIENS, GB:NP_004946[PUTATIVE] | Transporter |
| 16381 | 2059 | EQUILIBRATIVE NUCLEOSIDE TRANSPORTER 1, HOMO SAPIENS, GB:NP_004946[PUTATIVE] | Transporter |
| 16382 | 2060 | EQUILIBRATIVE NUCLEOSIDE TRANSPORTER 1, HOMO SAPIENS, GB:NP_004946[PUTATIVE] | Transporter |
| 16388 | 2061 | RECEPTOR PROTEIN KINASE - LIKE PROTEIN RECEPTOR-LIKE PROTEIN KINASE HOMOLOG RK20-1, PHAESOLUS VULGARIS, GB:AAD21872 | Kinase, Protein |
| 16404 | 2062 | GAG-PROTEASE · POLYPROTEIN, GLYCINE MAX., GB:AAC18777[PUTATIVE] | Protease |
| 16406 | 2063 | AAA FAMILY ATPASE BCS1P MITOCHONDRIAL, SACCHAROMYCES CEREVISIAE, SWISS PROT:P32839[PUTATIVE] | ATPase |
| 16407 | 2064 | FERREDOXIN--NADP+ REDUCTASE - LIKE PROTEIN FERREDOXIN--NADP+ REDUCTASE, PISUM SATIVUM, PIR:T06773 | Reductase |
| 16411 | 2065 | GLUCAN ENDO-1,3-BETA-GLUCOSIDASE PRECURSOR, TRITICUM AESTIVUM, U30323[PUTATIVE] | Glycosylase |
| 16479 | 2066 | REVERSE TRANSCRIPTASE [PUTATIVE] | Transcriptase |
| 16501 | 2067 | GLUCOSYLTRANSFERASE [PUTATIVE] | Transferases |
| 16516 | 2068 | XYLAN ENDOHYDROLASE [PUTATIVE] | Hydrolase |
| 16517 | 2069 | INOSITOL 1,3,4-TRISPHOSPHATE 5/6-KINASE-LIKE PROTEIN INOSITOL 1,3,4-TRISPHOSPHATE 5/6-KINASE (EC 2.7.-.-) - ARABIDOPSIS THALIANA, PIR2:JC5401 | Kinase |
| 16526 | 2070 | PROTEIN PHOSPHATASE 2C - MEDICAGO SATIVA, PID:E305311[PUTATIVE] | Phosphatase |
| 16539 | 2071 | ASCORBATE PEROXIDASE STROMAL | Oxidase |
| 16577 | 2072 | PEROXIDASE C2 PRECURSOR LIKE PROTEIN PEROXIDASE (EC 1.11.1.7) C2 PRECURSOR - ARMORACIA RUSTICANA, PID:D1014846 | Oxidase |
| 16578 | 2073 | PEROXIDASE C2 PRECURSOR LIKE PROTEIN PEROXIDASE (EC 1.11.1.7) C2 PRECURSOR - ARMORACIA RUSTICANA, PID:D1014846 | Oxidase |

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| 16583 | 2074 | REVERSE TRANSCRIPTASE OF ARABIDOPSIS THALIANA[PUTATIVE] | Transcriptase |
| 16586 | 2075 | ARGINASE SIMILAR TO ARGINASES (PFAM: PF00491, SCORE=353.2, E=1.4E-119, N=1)[PUTATIVE] | AMIDASE |
| 16589 | 2076 | ARGINASE | ARGINASE. |
| 16592 | 2077 | PROTEIN DISULFIDE ISOMERASE [PUTATIVE] | Isomerase |
| 16600 | 2078 | ASCORBATE PEROXIDASE - SPINACIA OLERACEA,PIR2:S66265[PUTATIVE] | Oxidase |
| 16601 | 2079 | ISOAMYLASE-LIKE PROTEIN PROBABLE ISOAMYLASE (EC 3.2.1.68) SU1 - ZEA MAYS,PIR2:T01321 | Glycosylase |
| 16608 | 2080 | BETA-1,3-GLUCANASE-LIKE PROTEIN PROBABLE BETA-1,3-GLUCANASE - TRITICUM AESTIVUM,PIR2:T06268 | Glycosylase |
| 16648 | 2081 | ANTHOCYANIN RHAMNOSYLTRANSFERASE -PETUNIA X HYBRIDA, PID:G454253[PUTATIVE] | Transferases |
| 16650 | 2082 | PHOSPHONOPYRUVATE DECARBOXYLASE (EC 4.1.1.-) - METHANOBACTERIUM THERMOAUTOTROPHICUM,PID:G2622714[PUTATIVE] | Decarboxylase |
| 16700 | 2083 | BETA-HYDROXYSTEROID DEHYDROGENASE (EC 1.1.1.146) I - MOUSE, PIR1:I56604[PUTATIVE] | Dehydrogenases |
| 16703 | 2084 | LIPASE-LIKE PROTEIN MONOGLYCERIDE LIPASE - MUS MUSCULUS, PID:E1184892 | Lipase |
| 16705 | 2085 | DNA-DIRECTED RNA POLYMERASE DNA-DIRECTED RNA POLYMERASE (EC 2.7.7.6) II LARGESTCHAIN - MOUSE, PIR2:A28490[PUTATIVE] | Polymerase |
| 16710 | 2086 | SUCROSE-PHOSPHATE SYNTHASE - LIKE PROTEIN SUCROSE-PHOSPHATE SYNTHASE, ZEA MAYS, PIR2:JQ1329 | Synthase |
| 16724 | 2087 | FRUCTOKINASE - LIKE PROTEIN FRUCTOKINASE, LYCOPERSICON ESCULENTUM, GB:U62329 | Kinase |
| 16729 | 2088 | POTASSIUM UPTAKE TRANSPORTER - LIKE PROTEIN POTASSIUM TRANSPORT PROTEIN TRK1, SACCHAROMYCES CEREVISIAE, PIR2:JU0466 | Transporter |
| 16737 | 2089 | CLV1 RECEPTOR KINASE, ARABIDOPSIS THALIANA, GB:U96879[PUTATIVE] | Kinase, Protein |

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| 16747 | 2090 | FLAVANONE 3-BETA-HYDROXYLASE NARINGENIN 3-DIOXYGENASE (EC 1.14.11.9) - CHINA ASTER, PIR2:S32147[PUTATIVE] | Oxygenases |
| 16748 | 2091 | FE(II)/ASCORBATE OXIDASE SRG1 PROTEIN - ARABIDOPSIS THALIANA, PIR2:S44261[PUTATIVE] | Oxidase |
| 16749 | 2092 | SUBTILISIN-LIKE PROTEASE SUBTILISIN-LIKE PROTEASE - LYCOPERSICON ESCULENTUM (TOMATO), PID:E1299610[PUTATIVE] | Protease |
| 16750 | 2093 | SUBTILISIN-LIKE PROTEASE SUBTILISIN-LIKE PROTEASE - LYCOPERSICON ESCULENTUM, PID:E1299610[PUTATIVE] | Protease |
| 16751 | 2094 | SUBTILISIN-LIKE PROTEASE SUBTILISIN-LIKE PROTEASE - LYCOPERSICON ESCULENTUM, PID:E1299610[PUTATIVE] | Protease |
| 16752 | 2095 | SUBTILISIN-LIKE PROTEASE SUBTILISIN-LIKE PROTEASE - LYCOPERSICON ESCULENTUM, PID:E1299610[PUTATIVE] | Protease |
| 16753 | 2096 | SUBTILISIN-LIKE PROTEASE -LIKE PROTEIN SUBTILISIN-LIKE PROTEASE AIR3 -ARABIDOPSIS THALIANA, PID:G3695019 | Protease |
| 16773 | 2097 | 2,4-DIHYDROXYHEPT-2-ENE-1,7-DIOIC ACID ALDOLASES FUNCTIONAL CATALOG ID=01.05[PUTATIVE] | Aldolase |
| 16775 | 2098 | OLIGOPEPTIDE TRANSPORTER SIMILAR TO C. ALBICANS OPT1, GENBANK ACCESSION NUMBER U60973 FUNCTIONAL CATALOG ID=07.99[PUTATIVE] | Transporter |
| 16790 | 2099 | RNA POLYMERASE II TRANSCRIPTION COFACTOR P15, HOMO SAPIENS, PIR2:A54670[PUTATIVE] | Polymerase |
| 16802 | 2100 | PROTEIN PHOSPHOPROTEIN PHOSPHATASE (EC 3.1.3.16) 2C - ARABIDOPSIS THALIANA, PIR2:S55457[PUTATIVE] | Phosphatase |
| 16827 | 2101 | PEROXIDASE ATP19A | Oxidase |
| 16842 | 2102 | MITOCHONDRIAL CARRIER PROTEIN - RIBES NIGRUM, PID:E1313696[PUTATIVE] | Transporter |

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| 16844 | 2103 | SERINE/THREONINE KINASE-LIKE PROTEIN RECEPTOR-LIKE PROTEIN KINASE RLK3 - ARABIDOPSIS THALIANA,PID:E1363211 | Kinase, Protein |
| 16845 | 2104 | SERINE/THREONINE KINASE-LIKE PROTEIN RECEPTOR-LIKE PROTEIN KINASE RLK3 - ARABIDOPSIS THALIANA,PID:E136321 | Kinase, Protein |
| 16846 | 2105 | SERINE/THREONINE KINASE-LIKE PROTEIN RECEPTOR-LIKE PROTEIN KINASE RLK3 - ARABIDOPSIS THALIANA,PID:E136321 | Kinase, Protein |
| 16847 | 2106 | SERINE/THREONINE KINASE-LIKE PROTEIN RECEPTOR-LIKE PROTEIN KINASE RLK3 - ARABIDOPSIS THALIANA,PID:E136321 | Kinase, Protein |
| 16848 | 2107 | SERINE/THREONINE KINASE-LIKE PROTEIN (FRAGMENT) RECEPTOR-LIKE PROTEIN KINASE RKS1 - ARABIDOPSIS THALIANA,PID:G4008008 | Kinase, Protein |
| 16850 | 2108 | RECEPTOR-LIKE PROTEIN KINASE RLK3 - ARABIDOPSIS THALIANA,PID:E136321[PUTATIVE] | Kinase, Protein |
| 16851 | 2109 | SERINE/THREONINE KINASE-LIKE PROTEIN (FRAGMENT) RECEPTOR-LIKE PROTEIN KINASE RLK3 - ARABIDOPSIS THALIANA,PID:E136321 | Kinase, Protein |
| 16855 | 2110 | BETA-PHOSPHOGLUCOMUTASE - LACTOBACILLUS SANFRANCISCO,PID:E1331347[PUTATIVE] | Mutase |
| 16859 | 2111 | PHOSPHORIBOSYLANTHRANILATE TRANSFERASE PHOSPHORIBOSYLANTHRANILATE TRANSFERASE, PISUM SATIVUM, D86180[PUTATIVE] | Transferases |
| 16869 | 2112 | REVERSE TRANSCRIPTASE /TRANSPOSON, ARABIDOPSIS THALIANA[PUTATIVE] | Transcriptase |
| 16881 | 2113 | PHOSPHOLIPASE D-GAMMA PHOSPHOLIPASE D- GAMMA - ARABIDOPSIS THALIANA,PID:G2653885[PUTATIVE] | Lipase |
| 16882 | 2114 | PHOSPHOLIPASE D-GAMMA PHOSPHOLIPASE D- GAMMA - ARABIDOPSIS THALIANA,PID:G2653885[PUTATIVE] | Lipase |
| 16883 | 2115 | PHOSPHOLIPASE D-GAMMA PHOSPHOLIPASE D- GAMMA - ARABIDOPSIS THALIANA,PID:G2653885[PUTATIVE] | Lipase |

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| 16887 | 2116 | PROTEIN KINASE - LIKE PROTEIN KI DOMAIN INTERACTING KINASE 1 -ZEA MAYS,PIR2:T02053 | Kinase, Protein |
| 16888 | 2117 | KI DOMAIN INTERACTING KINASE 1 -LIKE PROTEIN KI DOMAIN INTERACTING KINASE 1 - ZEA MAYS,PID:G2735017 | Kinase, Protein |
| 16901 | 2118 | TRANSPORT PROTEIN NA(+) DEPENDENT TRANSPORTER (SBF FAMILY) - AQUIFEX AEOLICUS, PIR2:E70482[PUTATIVE] | Transporter |
| 16923 | 2119 | NUCLEOTIDE SUGAR EPIMERASE -LIKE PROTEIN NUCLEOTIDE SUGAR EPIMERASE -VIBRIO VULNIFICUS,PID:G3093975 | Epimerase |
| 16925 | 2120 | COPPER AMINE OXIDASE LIKE PROTEIN (FRAGMENT1) COPPER AMINE OXIDASE - CICERARIETINUM,PID:E1335964 | Oxidase |
| 16926 | 2121 | COPPER AMINE OXIDASE LIKE PROTEIN (FRAGMENT2) COPPER AMINE OXIDASE - CICERARIETINUM,PID:E1335964 | Oxidase |
| 16937 | 2122 | PECTINESTERASE - CITRUS SINENSIS,PID:G2098711[PUTATIVE] | Esterase |
| 16941 | 2123 | TREHALOSE-6-PHOSPHATE PHOSPHATASE (ATTPPA) TREHALOSE-6-PHOSPHATE PHOSPHATASE - ARABIDOPSIS THALIANA, PID:G2944178[PUTATIVE] | Phosphatase |
| 16980 | 2124 | HYDROLASE-LIKE PROTEIN 2-HYDROXY-6-OXOHEPTA-2,4-DIENOATE HYDROLASE (EC 3.7.-.-) - SYNECHOCYSTIS SP., PIR2:S77427 | Hydrolase |
| 16998 | 2125 | OXIDOREDUCTASE - STREPTOMYCES LIVIDANS,PID:G3293547[PUTATIVE] | Reductase |
| 17002 | 2126 | OLEOYL-[ACYL-CARRIER-PROTEIN] HYDROLASE-LIKE PROTEIN OLEOYL-[ACYL-CARRIER-PROTEIN] HYDROLASE - BRASSICA NAPUS, PIR2:S40407 | Hydrolase |
| 17005 | 2127 | ENDOXYLOGLUCAN TRANSFERASE-LIKE PROTEIN XYLOGLUCAN ENDO-1,4-BETA-D-GLUCANASE (EC 3.2.1.-) - ARABIDOPSIS THALIANA,PIR2:C49539 | Transferases |
| 17006 | 2128 | ENDOXYLOGLUCAN TRANSFERASE-LIKE PROTEIN XYLOGLUCAN ENDO-1,4-BETA-D-GLUCANASE (EC 3.2.1.-) - ARABIDOPSIS THALIANA,PIR2:C49539 | Transferases |

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| 17015 | 2129 | SHORT-CHAIN ALCOHOL DEHYDROGENASE LIKE PROTEIN SHORT-CHAIN ALCOHOL DEHYDROGENASE - PICEA ABIES, PIR2:S34678 | Dehydrogenase |
| 17018 | 2130 | PECTATE LYASE LIKE PROTEIN PECTATE LYASE - FRAGARIA X ANANASSA,PID:G2435395 | Lyase |
| 17023 | 2131 | DIMETHYLANILINE MONOOXYGENASE (N-OXIDE- FORMING) (EC1.14.13.8) -ORYCTOLAGUS CUNICULUS,PID:G164989[PUTATIVE] | Oxygenases |
| 17027 | 2132 | TERPENE SYNTHASE TS1, ARABIDOPSIS THALIANA, Y11188[PUTATIVE] | Synthase |
| 17038 | 2133 | CYCLIC BETA-1-3-GLUCAN SYNTHASE, BRADYRHIZOBIUM JAPONICUM, AF047687[PUTATIVE] | Synthase |
| 17039 | 2134 | POTASSIUM TRANSPORTER - LIKE PROTEIN POTASSIUM TRANSPORTER ATK1P, ARABIDOPSIS THALIANA,AF012656 | Transporter |
| 17040 | 2135 | 3-ISOPROPYLMALATE DEHYDRATASES/ACONITATE HYDRATASES[PUTATIVE] | Dehydratase |
| 17057 | 2136 | BETA 1,3-GLUCANASE, TRITICUM AESTIVUM, U30323[PUTATIVE] | Glycosylase |
| 17063 | 2137 | ISOFLAVONE REDUCTASE-LIKE PROTEIN ISOFLAVONE REDUCTASE-LIKE PROTEIN, LUPINUS ALBUS, GB:U48590 | Reductase |
| 17067 | 2138 | PURPLE ACID PHOSPHATASE IPOMOEA BATATAS, AJ006224[PUTATIVE] | Phosphatase |
| 17068 | 2139 | PECTATE LYASE A11 (FRAGMENT) [PUTATIVE] | Lyase |
| 17073 | 2140 | POLYGALACTURONASE POLYGALACTURONASE, ZEA MAYS, PIR2:S30067[PUTATIVE] | Glycosylase |
| 17106 | 2141 | GLUCOSYLTRANSFERASE LIKE PROTEIN | Transferases |
| 17110 | 2142 | XYLOGLUCAN ENDOTRANSGLYCOSYLASE-RELATED PROTEIN XTR-7 | Glycosylase |
| 17118 | 2143 | PHYTOENE DESATURASE, PHYTOENE DEHYDROGENASE PRECURSOR | Desaturases |
| 17140 | 2144 | CARNITINE RACEMASE LIKE PROTEIN | Epimerase |
| 17141 | 2145 | CARNITINE RACEMASE LIKE PROTEIN | Epimerase |
| 17144 | 2146 | REVERSE TRANSCRIPTASE LIKE PROTEIN | Transcriptase |

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| 17154 | 2147 | ACYLAMINOACYL-PEPTIDASE LIKE PROTEIN | Protease |
| 17160 | 2148 | GERMIN PRECURSOR OXALATE OXIDASE | Oxidase |
| 17163 | 2149 | RNA POLYMERASE II FIFTH LARGEST SUBUNIT LIKE PROTEIN | Polymerase |
| 17188 | 2150 | IMIDAZOLEGLYCEROL-PHOSPHATE DEHYDRATASE | Dehydratase |
| 17218 | 2151 | ABC TRANSPORTER HOMOLOG | Transporter |
| 17222 | 2152 | GLUCOSYLTRANSFERASE | Transferases |
| 17223 | 2153 | UTP-GLUCOSE GLUCOSYLTRANSFERASE LIKE PROTEIN | Transferases |
| 17224 | 2154 | UTP-GLUCOSE GLUCOSYLTRANSFERASE | Transferases |
| 17225 | 2155 | CELLULOSE SYNTHASE LIKE PROTEIN | Synthase |
| 17228 | 2156 | CELLULOSE SYNTHASE LIKE PROTEIN | Synthase |
| 17240 | 2157 | HYDROPEROXIDE LYASE (HPOL) LIKE PROTEIN | Lyase |
| 17244 | 2158 | INDOLE-3-ACETATE BETA-GLUCOSYLTRANSFERASE LIKE PROTEIN | Transferases |
| 17245 | 2159 | INDOLE-3-ACETATE BETA-GLUCOSYLTRANSFERASE LIKE PROTEIN | Transferases |
| 17246 | 2160 | INDOLE-3-ACETATE BETA-GLUCOSYLTRANSFERASE LIKE PROTEIN | Transferases |
| 17249 | 2161 | PYRUVATE PHOSPHATE DIKINASE, PYRUVATE, ORTHOPHOSPHATE DIKINASE | Kinase |
| 17251 | 2162 | GLUCOSYLTRANSFERASE LIKE PROTEIN | Transferases |
| 17261 | 2163 | KINASE LIKE PROTEIN | Kinase, Protein |
| 17283 | 2164 | DELTA-CADINENE SYNTHASE LIKE PROTEIN | Synthase |
| 17294 | 2165 | PECTINESTERASE LIKE PROTEIN | Esterase |
| 17309 | 2166 | GALACTOKINASE LIKE PROTEIN | Kinase |
| 17322 | 2167 | BETA-1,3-GLUCANASE CLASS I PRECURSOR | Glycosylase |
| 17323 | 2168 | PEROXIDASE LIKE PROTEIN | Oxidase |
| 17327 | 2169 | NARINGENIN 3-DIOXYGENASE LIKE PROTEIN | Oxygenases |
| 17353 | 2170 | CELLULOSE SYNTHASE LIKE PROTEIN | Synthase |
| 17354 | 2171 | GLUCOSYLTRANSFERASE LIKE PROTEIN | Transferases |
| 17363 | 2172 | CYANOHYDRIN LYASE LIKE PROTEIN | Lyase |
| 17367 | 2173 | LIMONENE CYCLASE LIKE PROTEIN | Cyclase |
| 17368 | 2174 | LIMONENE CYCLASE LIKE PROTEIN | Cyclase |

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| 17371 | 2175 | GIBBERELLIN OXIDASE-LIKE PROTEIN | Oxidase |
| 17376 | 2176 | TRIACYLGLYCEROL LIPASE LIKE PROTEIN | Lipase |
| 17390 | 2177 | KINASE LIKE PROTEIN | Kinase, Protein |
| 17402 | 2178 | BETA-AMYLASE [PUTATIVE] | Glycosylase |
| 17403 | 2179 | SERINE PROTEASE-LIKE PROTEIN [PUTATIVE] | Protease |
| 17427 | 2180 | PHOSPHORIBOSYLGLYCINAMIDE FORMYLTRANSFERASE-LIKE PROTEIN | Transferases |
| 17464 | 2181 | PEROXIDASE LIKE PROTEIN | Oxidase |
| 17477 | 2182 | N-ACETYLORNITHINE DEACETYLASE-LIKE PROTEIN, FRAGMENT N-ACETYLORNITHINE DEACETYLASE (AODD) - DICTYOSTELIUM DISCOIDEUM, PID:G763048 | |
| 17510 | 2183 | POTASSIUM CHANNEL - LIKE PROTEIN KCO1, ARABIDOPSIS THALIANA, Y07825 | Channel |
| 17512 | 2184 | POLYGALACTURONASE-LIKE PROTEIN EXOPOLYGALACTURONASE, ARABIDOPSIS THALIANA, PIR2:S34266 | Glycosylase |
| 17518 | 2185 | STARCH SYNTHASE-LIKE PROTEIN BACTERIAL AND PLANT GLYCOGEN (STARCH) SYNTHASES; FOR EXAMPLE B.SUBTILIS, PATCHX:D1020368 | Synthase |
| 17519 | 2186 | RECEPTOR SERINE/THREONINE KINASE-LIKE PROTEIN RECEPTOR SERINE/THREONINE KINASE PR5K, PATCHX:G1235680 | Kinase, Protein |
| 17521 | 2187 | PHOSPHO-N-ACETYLMURAMOYL-PENTAPEPTIDE- TRANSFERASE, HAEMOPHILUS INFLUENZAE, PIR2:A64185[PUTATIVE] | Transferases |
| 17523 | 2188 | POTASSIUM CHANNEL PROTEIN KAT2 | Channel |
| 17528 | 2189 | BETA-1,3-GLUCANASE-LIKE PROTEIN STRONG SIMILARITY TO ENDO-BETA-1,3-BETA-D- GLUCOSIDASE, NICOTIANA TABACUM, PIR2:S46495 | Glycosylase |
| 17538 | 2190 | ADENYLOSUCCINATE LYASE - LIKE PROTEIN ADENYLOSUCCINATE LYASE - HAEMOPHILUS INFLUENZAE | Lyase |
| 17549 | 2191 | LIPASE-LIKE PROTEIN PN47P, IPOMOEA NIL, PID:G1527001 | Lipase |
| 17572 | 2192 | CELLULOSE SYNTHASE - LIKE PROTEIN CELLULOSE SYNTHASE, GOSSYPIUM HIRSUTUM, U58283 | Synthase |

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| 17576 | 2193 | DNA POLYMERASE III HOLOENZYME TAU SUBUNIT, THERMUS THERMOPHILUS, GB:AF025391[PUTATIVE] | Polymerase |
| 17589 | 2194 | PROTEIN KINASE - LIKE PROTEIN PROTEIN KINASE 6, GLYCINE MAX., PIR2:S29851 | Kinase, Protein |
| 17593 | 2195 | XYLOGLUCAN ENDO-TRANSGLYCOSYLASE - LIKE PROTEIN XYLOGLUCAN ENDO-TRANSGLYCOSYLASE RELATED PROTEIN XTR-4, ARABIDOPSIS THALIANA, PIR2:S71223 | Glycosylase |
| 17596 | 2196 | DNA (CYTOSINE-5-)-METHYLTRANSFERASE, ARABIDOPSIS THALIANA, PIR2:S59604[PUTATIVE] | Transferases |
| 17635 | 2197 | PECTINACETYLESTERASE PROTEIN PECTINACETYLESTERASE PRECURSOR, VIGNA RADIATA, PIR2:S68805[PUTATIVE] | Esterase |
| 17636 | 2198 | PECTINACETYLESTERASE PECTINACETYLESTERASE PRECURSOR, VIGNA RADIATA, PIR2:S68805[PUTATIVE] | Esterase |
| 17662 | 2199 | FE(II) TRANSPORT PROTEIN FE(II) TRANSPORT PROTEIN, ARABIDOPSIS THALIANA, GB:U27590[PUTATIVE] | Transporter |
| 17663 | 2200 | FE(II) TRANSPORT PROTEIN | Transporter |
| 17665 | 2201 | ASPARTATE KINASE-HOMOSERINE DEHYDROGENASE - LIKE PROTEIN AK-HSDH BIFUNCTIONAL ENZYME PRECURSOR, ARABIDOPSIS THALIANA, PIR2:S46497 | Dehydrogenases |
| 17666 | 2202 | CHITINASE / LYSOZYME PZ PRECURSOR, NICOTIANA TABACUM, PIR2:S51591[PUTATIVE] | Chitinase |
| 17668 | 2203 | CHITINASE / LYSOZYME PZ PRECURSOR, NICOTIANA TABACUM, PIR2:S51591[PUTATIVE] | Chitinase |
| 17677 | 2204 | PEPTIDYL-PROLYL CIS-TRANS ISOMERASE FKBP-TYPE, SYNECHOCYSTIS SP., PIR2:S75144[PUTATIVE] | Isomerase |
| 17688 | 2205 | POTASSIUM TRANSPORTER-LIKE PROTEIN PUTATIVE POTASSIUM TRANSPORTER ATKT2P & ATKT1P, ARABIDOPSIS THALIANA, PATCHX:G2384669 & PATCHX:G2384671 | Transporter |
| 17700 | 2206 | PHOSPHORIBOSYLANTHRANILATE TRANSFERASE PHOSPHORIBOSYLANTHRANILATE TRANSFERASE, PARTIAL CDS, PISUM SATIVUM, PATCHX:D1013719 | Transferases |

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| 17703 | 2207 | VACUOLAR SORTING RECEPTOR-LIKE PROTEIN BP-80 VACUOLAR SORTING RECEPTOR, PISUM SATIVUM, PATCHX:G1737222 | Receptor |
| 17712 | 2208 | TERPENE CYCLASE LIKE PROTEIN 5-EPI- ARISTOLOCHENE SYNTHASE, NICOTIANA TABACUM, PATX:G505588 | Cyclase |
| 17713 | 2209 | CADINENE SYNTHASE LIKE PROTEIN (+)-DELTA- CADINENE SYNTHASE ISOZYME XC14, GOSSYPIMUM ARBOREUM, PIR2:S68366 | Synthase |
| 17715 | 2210 | TERPENE CYCLASE LIKE PROTEIN VETISPIRADIENE SYNTHASE, HYOSCYAMUS MUTICUS, PATX:G763421 | Cyclase |
| 17719 | 2211 | CLV1 RECEPTOR KINASE LIKE PROTEIN CLAVATA1 RECEPTOR KINASE, ARABIDOPSIS TH., PATX:G2160756 | Kinase, Protein |
| 17744 | 2212 | RNA-DIRECTED DNA POLYMERASE, ARABIDOPSIS THALIANA, PIR:S65815[PUTATIVE] | Polymerase |
| 17745 | 2213 | PROTEIN KINASE LIKE PROTEINS, ARABIDOPSIS[PUTATIVE] | Kinase, Protein |
| 17746 | 2214 | RECEPTOR-LIKE PROTEIN KINASE HOMOLOG RK20-1, PHASEOLUS VULGARIS, GB:AF078082[PUTATIVE] | Kinase, Protein |
| 17747 | 2215 | RECEPTOR-LIKE PROTEIN KINASE HOMOLOG RK20-1, PHASEOLUS VULGARIS, GB:AF078082[PUTATIVE] | Kinase, Protein |
| 17748 | 2216 | RECEPTOR-LIKE PROTEIN KINASE HOMOLOG RK20-1, PHASEOLUS VULGARIS, GB:AF078082[PUTATIVE] | Kinase, Protein |
| 17749 | 2217 | RECEPTOR-LIKE PROTEIN KINASE HOMOLOG RK20-1, PHASEOLUS VULGARIS, GB:AF078082[PUTATIVE] | Kinase, Protein |
| 17750 | 2218 | RECEPTOR-LIKE PROTEIN KINASE HOMOLOG RK20-1, PHASEOLUS VULGARIS, GB:AF078082[PUTATIVE] | Kinase, Protein |
| 17751 | 2219 | RECEPTOR-LIKE PROTEIN KINASE HOMOLOG RK20-1, PHASEOLUS VULGARIS, GB:AF078082[PUTATIVE] | Kinase, Protein |
| 17752 | 2220 | RECEPTOR-LIKE PROTEIN KINASE HOMOLOG RK20-1, PHASEOLUS VULGARIS, GB:AF078082[PUTATIVE] | Kinase, Protein |
| 17753 | 2221 | RECEPTOR-LIKE PROTEIN KINASE HOMOLOG RK20-1, PHASEOLUS VULGARIS, GB:AF078082[PUTATIVE] | Kinase, Protein |
| 17754 | 2222 | RECEPTOR-LIKE PROTEIN KINASE HOMOLOG RK20-1, PHASEOLUS VULGARIS, GB:AF078082[PUTATIVE] | Kinase, Protein |

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| 17755 | 2223 | RECEPTOR-LIKE PROTEIN KINASE HOMOLOG RK20-1, PHASEOLUS VULGARIS, GB:AF078082[PUTATIVE] | Kinase, Protein |
| 17756 | 2224 | RECEPTOR-LIKE PROTEIN KINASE HOMOLOG RK20-1, PHASEOLUS VULGARIS, GB:AF078082[PUTATIVE] | Kinase, Protein |
| 17757 | 2225 | PROTEIN (FRAGMENT) RECEPTOR-LIKE PROTEIN KINASE HOMOLOG RK20-1, PHASEOLUS VULGARIS, GB:AF078082[PUTATIVE] | Kinase, Protein |
| 17758 | 2226 | RECEPTOR-LIKE PROTEIN KINASE, RLK3, ARABIDOPSIS THALIANA, AJ011674[PUTATIVE] | Kinase, Protein |
| 17759 | 2227 | PROTEIN KINASE LIKE PROTEINS, ARABIDOPSIS[PUTATIVE] | Kinase, Protein |
| 17761 | 2228 | PROTEIN KINASE LIKE PROTEINS, ARABIDOPSIS THALIANA[PUTATIVE] | Kinase, Protein |
| 17762 | 2229 | PROTEIN KINASE LIKE PROTEINS, ARABIDOPSIS[PUTATIVE] | Kinase, Protein |
| 17770 | 2230 | RECEPTOR-LIKE PROTEIN KINASE, RLK3, ARABIDOPSIS THALIANA, AJ011674[PUTATIVE] | Kinase, Protein |
| 17773 | 2231 | RETICULINE OXIDASE - LIKE PROTEIN RETICULINE OXIDASE (EC 1.5.3.9) PRECURSOR, ESCHSCHOLZIA CALIFORNICA, PIR2:A41533 | Oxidase |
| 17774 | 2232 | RETICULINE OXIDASE -LIKE PROTEIN RETICULINE OXIDASE, ESCHSCHOLZIA CALIFORNICA, PIR:A41533 | Oxidase |
| 17775 | 2233 | RETICULINE OXIDASE - LIKE PROTEIN RETICULINE OXIDASE PRECURSOR, ESCHSCHOLZIA CALIFORNICA, PIR:A41533 | Oxidase |
| 17776 | 2234 | TRIPEPTIDYL-PEPTIDASE II, HOMO SAPIENS, PIR:S54376[PUTATIVE] | Protease |
| 17785 | 2235 | RECEPTOR KINASE-LIKE GENE, ORYZA LONGISTAMINATA, GB:U72725[PUTATIVE] | Kinase, Protein |
| 17790 | 2236 | CARBONIC ANHYDRASE -LIKE PROTEIN CARBONIC ANHYDRASE, ARABIDOPSIS THALIANA, GB:U73462 | Anhydrase |
| 17791 | 2237 | CARBONIC ANHYDRASE - LIKE PROTEIN DIOSCORIN CLASS A PRECURSOR, DIOSCOREA CAYENENSIS, PIR:S57766 | Anhydrase |

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| 17811 | 2238 | GIBBERELLIN 20-OXIDASE - LIKE PROTEIN GIBBERELLIN C-20 OXIDASE, ORYZA SATIVA, PATCHX:G1854637 | Oxidase |
| 17813 | 2239 | UDP-3-O-[3-HYDROXYMYRISTOYL] GLUCOSAMINE N- ACYLTRANSFERASE, E.COLI, PIR2:S13729[PUTATIVE] | Transferases |
| 17814 | 2240 | RECEPTOR KINASE - LIKE PROTEIN SRK3 RECEPTOR KINASE, BRASSICA OLERACEA, PATCHX:G624943 | Kinase, Protein |
| 17827 | 2241 | RECEPTOR KINASE - LIKE PROTEIN RECEPTOR-LIKE KINASE SFR2, BRASSICA OLERACEA, PID:E258943 | Kinase, Protein |
| 17828 | 2242 | RECEPTOR-LIKE SERINE/THREONINE PROTEIN KINASE ARK3 | Kinase, Protein |
| 17829 | 2243 | SERINE/THREONINE KINASE - LIKE PROTEIN SERINE/THREONINE KINASE BRLK, BRASSICA OLERACEA, GB:Y12531 | Kinase, Protein |
| 17830 | 2244 | SERINE/THREONINE PROTEIN KINASE - LIKE PROTEIN RECEPTOR PROTEIN KINASE (IRK1), IPOMOEA TRIFIDA, GB:U20948 | Kinase, Protein |
| 17831 | 2245 | SERINE/THREONINE KINASE - LIKE PROTEIN | Kinase, Protein |
| 17839 | 2246 | NADH DEHYDROGENASE LIKE PROTEIN NADH DEHYDROGENASE (UBIQUINONE) (EC 1.6.5.3)CHAIN NDII YEAST,PIR2:S26704 AND OTHER NADH DEHYDROGENASES | Dehydrogenase |
| 17849 | 2247 | BIFUNCTIONAL NUCLEASE, ZINNIA ELEGANS, GB:U90266[PUTATIVE] | Nuclease |
| 17850 | 2248 | BIFUNCTIONAL NUCLEASE D, ZINNIA ELEGANS, GB:U90266[PUTATIVE] | Nuclease |
| 17853 | 2249 | SERINE PROTEASE - LIKE PROTEIN CUCUMISIN, CUCUMIS MELO, A55800 | Protease |
| 17854 | 2250 | SUBTILISIN-LIKE PROTEASE SUBTILISIN-LIKE PROTEASE - LYCOPERSICON ESCULENTUM,AJ006378 | Protease |
| 17858 | 2251 | PEPTIDE TRANSPORTER - LIKE PROTEIN PEPTIDE TRANSPORTER (PTR1) - HORDEUM VULGARE,AF023472 | Transporter |
| 17859 | 2252 | GIBBERELLIN 3 BETA-HYDROXYLASE - LIKE PROTEIN 3B-HYDROXYLASE, SOLANUM LYCOPERSICUM, AB010992 | Hydroxylase |
| 17886 | 2253 | PEROXIDASE PRXR1 | Oxidase |

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| 17891 | 2254 | PECTINESTERASE LIKE PROTEIN PECTINESTERASE, LYCOPERSICON ESCULENTUM, PATX:E312172 | Esterase |
| 17898 | 2255 | PECTATE LYASE LIKE PROTEIN PECTATE LYASE, ZINNIA ELEGANS, PATX:E283787 | Lyase |
| 17899 | 2256 | PECTATE LYASE LIKE PROTEIN PECTATE LYASE, ZINNIA ELEGANS, PATX:E283787 | Lyase |
| 17903 | 2257 | SERINE/THREONINE PROTEIN KINASE LIKE PROTEIN SERINE/THREONINE PROTEIN KINASE (ARSK1 GENE), ARABIDOPSIS THALIANA, PATCHX:G1066501 | Kinase, Protein |
| 17904 | 2258 | RECEPTOR LIKE PROTEIN (FRAGMENT) ES43 PROTEIN, BARLEY, PIR2:S44281 | Receptor |
| 17916 | 2259 | ALTERNATIVE OXIDASE, MANGIFERA INDICA, PIR2:S45035[PUTATIVE] | Oxidase |
| 17949 | 2260 | TREHALOSE-6-PHOSPHATE PHOSPHATASE - LIKE PROTEIN TREHALOSE-6-PHOSPHATE PHOSPHATASE (ATTPPA), PID:G2944178 | Phosphatase |
| 17963 | 2261 | LEUCINE RICH REPEAT RECEPTOR KINASE-LIKE PROTEIN LEUCINE RICH REPEAT RECEPTOR-LIKE KINASE, ORYZA SATIVA, PATCHX:E267533 | Kinase, Protein |
| 17974 | 2262 | BILE ACID SODIUM-DEPENDENT TRANSPORTER, HOMO SAPIENS, PIR2:I38655, PREDICTED PROTEIN ILEAL | Transporter |
| 17977 | 2263 | ANTHOCYANIDIN SYNTHASE - LIKE PROTEIN PUTATIVE LEUCOANTHOCYANIDIN DIOXYGENASE, ARABIDOPSIS THALIANA, PID:G1575699 | Oxygenases |
| 17978 | 2264 | LEUCOANTHOCYANIDIN DIOXYGENASE (LDOX) [PUTATIVE] | Oxygenases |
| 18000 | 2265 | GAMMA-GLUTAMYL-CYSTEINE SYNTHETASE | Synthase |
| 18003 | 2266 | PROTEIN KINASE - LIKE PROTEIN SERINE/THREONINE KINASE - BRASSICA OLERACEA | Kinase, Protein |
| 18004 | 2267 | SERINE/THREONINE KINASE - LIKE PROTEIN KINASE DOMAIN INTERACTING KINASE 1 (KIK1), ZEA MAYS | Kinase, Protein |
| 18005 | 2268 | SERINE/THREONINE KINASE - LIKE PROTEIN KINASE DOMAIN INTERACTING KINASE 1 (KIK1), ZEA MAYS | Kinase, Protein |
| 18008 | 2269 | SERINE/THREONINE KINASE -LIKE PROTEIN SERINE/THREONINE KINASE, BRASSICA OLERACEA | Kinase, Protein |

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| 18009 | 2270 | SERINE/THREONINE KINASE - LIKE PROTEIN SERINE/THREONINE KINASE, BRASSICA OLERACEA | Kinase, Protein |
| 18010 | 2271 | SERINE /THREONINE KINASE - LIKE PROTEIN SERINE /THREONINE KINASE, BRASSICA OLERACEA | Kinase, Protein |
| 18011 | 2272 | SERINE/THREONINE KINASE - LIKE PROTEIN SERINE/THREONINE KINASE, BRASSICA OLERACEA | Kinase, Protein |
| 18012 | 2273 | SERINE/THREONINE KINASE - LIKE PROTEIN SERINE/THREONINE KINASE, BRASSICA OLERACEA | Kinase, Protein |
| 18013 | 2274 | S-RECEPTOR KINASE 8 PRECURSOR, BRASSICA CAMPESTRIS, PIR1:JC2481[PUTATIVE] | Kinase, Protein |
| 18014 | 2275 | SERINE/THREONINE KINASE - LIKE PROTEIN SERINE/THREONINE KINASE, BRASSICA OLERACEA | Kinase, Protein |
| 18015 | 2276 | PROTEIN KINASE - LIKE PROTEIN RECEPTOR KINASE 1, BRASSICA RAPA | Kinase, Protein |
| 18016 | 2277 | RECEPTOR PROTEIN KINASE, IPOMOEA TRIFIDA[PUTATIVE] | Kinase, Protein |
| 18017 | 2278 | SERINE/THREONINE KINASE SERINE/THREONINE KINASE, BRASSICA OLERACEA | Kinase, Protein |
| 18018 | 2279 | SERINE /THREONINE KINASE - LIKE PROTEIN SERINE /THREONINE KINASE, BRASSICA OLERACEA | Kinase, Protein |
| 18019 | 2280 | SERINE/THREONINE KINASE - LIKE PROTEIN SERINE/THREONINE KINASE, BRASSICA OLERACEAE | Kinase, Protein |
| 18020 | 2281 | SERINE/THREONINE KINASE - LIKE PROTEIN KI DOMAIN INTERACTING KINASE 1 (KIK1), ZEA MAYS | Kinase, Protein |
| 18021 | 2282 | SERINE/THREONINE KINASE - LIKE PROTEIN KI DOMAIN INTERACTING KINASE 1, ZEA MAYS | Kinase, Protein |
| 18022 | 2283 | SERINE/THREONINE KINASE - LIKE PROTEIN SERINE/THREONINE KINASE, BRASSICA OLERACEA | Kinase, Protein |
| 18024 | 2284 | ACC OXIDASE, NICOTIANA GLUTINOSA[PUTATIVE] | Oxidase |
| 18054 | 2285 | POTASSIUM TRANSPORT PROTEIN (TRH1) HIGH- AFFINITY POTASSIUM TRANSPORT PROTEIN KUP1, ARABIDOPSIS THALIANA, EMBL:AC004165[PUTATIVE] | Transporter |
| 18061 | 2286 | V-ATPASE SUBUNIT G (VAG2 GENE) | ATPase |
| 18064 | 2287 | RECEPTOR KINASE RECEPTOR-LIKE PROTEIN KINASE - ARABIDOPSIS THALIANA RKL1, PID:G4008006[PUTATIVE] | Kinase, Protein |

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| 18072 | 2288 | POLYGALACTURONASE POLYGALACTURONASE (EC 3.2.1.15) - AVOCADO, EMBL:X66426[PUTATIVE] | Glycosylase |
| 18089 | 2289 | CELLULOSE SYNTHASE CATALYTIC SUBUNIT - LIKE PROTEIN CELLULOSE SYNTHASE CATALYTIC SUBUNIT (ATH-A), ARABIDOPSIS THALIANA, GB:AF027173 | Synthase |
| 18090 | 2290 | CELLULOSE SYNTHASE CATALYTIC SUBUNIT, ARABIDOPSIS THALIANA, GB:AF027173[PUTATIVE] | Synthase |
| 18091 | 2291 | CELLULOSE SYNTHASE CATALYTIC SUBUNIT (ATH-A), ARABIDOPSIS THALIANA; GB:AF027173[PUTATIVE] | Synthase |
| 18098 | 2292 | 2,4-DIHYDROXYHEPT-2-ENE-1,7-DIOIC ACID ALDOLASE -ESCHERICHIA COLI,PID:G633197[PUTATIVE] | Aldolase |
| 18104 | 2293 | HYDROXYMUCONIC SEMIALDEHYDE HYDROLASE, PSEUDOMONAS STUTZERI, AF039534[PUTATIVE] | Hydrolase |
| 18128 | 2294 | DIHYDROFOLATE REDUCTASE - SCHIZOSACCHAROMYCES POMBE,PID:E1320950[PUTATIVE] | Reductase |
| 18155 | 2295 | TRNA ISOPENTENYLTRANSFERASE TRNA ISOPENTENYLTRANSFERASE (EC 2.5.1.8), YEAST (SACCHAROMYCES CEREVISIAE), PIR2:S67176[PUTATIVE] | Transferases |
| 18157 | 2296 | ALLIIN LYASE ALLIIN LYASE (EC 4.4.1.4) PRECURSOR (CYSTEINE SULPHOXIDE LYASE), ONION, PIR2:S29301[PUTATIVE] | Lyase |
| 18168 | 2297 | PECTATE LYASE PECTATE LYASE, MUSA ACUMINATA, PATX:E209876[PUTATIVE] | Lyase |
| 18169 | 2298 | DNA POLYMERASE III LIKE PROTEIN DNA POLYMERASE III GAMMA SUBUNIT - AQUIFEX AEOLICUS, PIR2:A70460 | Polymerase |
| 18171 | 2299 | ABC-TYPE TRANSPORT PROTEINS[PUTATIVE] | Transporter |
| 18178 | 2300 | ACID PHOSPHATASE (EC 3.1.3.2) PAP, PHASEOLUS VULGARIS, PIR1:S51031[PUTATIVE] | Phosphatase |
| 18189 | 2301 | ALPHA-AMYLASE - LIKE PROTEIN ALPHA-AMYLASE, VIGNA MUNGO, PIR2:S10514 | Glycosylase |

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| 18197 | 2302 | MAGNESIUM-PROTOPORPHYRIN METHYLTRANSFERASE - LIKE PROTEIN MAGNESIUM- PROTOPORPHYRIN IX METHYLTRANSFERASE, SYNECHOCYSTIS SP, PIR2:S71781 | IX Transferases |
| 18199 | 2303 | SUPEROXIDE DISMUTASE (EC 1.15.1.1) (FE)(FRAGMENT) | Mutase |
| 18204 | 2304 | ACID PHOSPHATASE - LIKE PROTEIN ACID PHOSPHATASE-1,LYCOPERSICON ESCULENTUM, SWISS-PROT:P27061 | Phosphatase |
| 18214 | 2305 | PECTINESTERASE GROUP I CITRUS SINENSIS, PID:G2098705[PUTATIVE] | Esterase |
| 18215 | 2306 | PECTINESTERASE - CITRUS SINENSIS, PID:G2098705[PUTATIVE] | Esterase |
| 18219 | 2307 | SRG1-LIKE PROTEIN STRONG HOMOLOGY TO SRG1 PROTEIN, A NEW MEMBER OF THE FE(II)/ASCORBATE OXIDASE SUPERFAMILY, PID:G479047 | Oxidase |
| 18220 | 2308 | SRG1-LIKE PROTEIN STRONG HOMOLOGY TO SRG1 PROTEIN, A NEW MEMBER OF THE FE(II)/ASCORBATE OXIDASE SUPERFAMILY, PID:G479047 | Oxidase |
| 18226 | 2309 | CLPC PROTEASE - SPINACIA OLERACEA,PID:G4105131[PUTATIVE] | Protease |
| 18228 | 2310 | RECEPTOR KINASE-LIKE PROTEIN RECEPTOR-LIKE PROTEIN KINASE, RLK3 - ARABIDOPSIS THALIANA,PID:E1363211 | Kinase, Protein |
| 18231 | 2311 | GIBBERELLIN 20-OXIDASE - ARABIDOPSIS THALIANA | Oxidase |
| 18259 | 2312 | BETA-CAROTENE HYDROXYLASE | Hydroxylase |
| 18261 | 2313 | GLUTAMINE CYCLOTRANSFERASE PRECURSOR - LIKE PROTEIN GLUTAMINE CYCLOTRANSFERASE PRECURSOR, CARICA PAPAYA, AF061240 | Transferases |
| 18270 | 2314 | XYLOGLUCAN ENDO-1,4-BETA-D-GLUCANASE (XTR-6) | Glycosylase |
| 18271 | 2315 | XYLOGLUCAN ENDO-1,4-BETA-D-GLUCANASE XYLOGLUCAN ENDO-1,4-BETA-D-GLUCANASE (EC 3.2.1.-) XTR-3 - ARABIDOPSIS THALIANA (FRAGMENT), PIR2:S71222[PUTATIVE] | Glycosylase |

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| 18284 | 2316 | V-ATPASE G-SUBUNIT LIKE PROTEIN G SUBUNIT OF VACUOLAR-TYPE H ⁺ -ATPASE (VAG1) - ARABIDOPSIS THALIANA, PID:E1330303 | ATPase |
| 18286 | 2317 | PHOSPHATIDYL SERINE DECARBOXYLASE PHOSPHATIDYL SERINE DECARBOXYLASE (EC 4.1.1.65) 2 - YEAST, PIR2:S64484[PUTATIVE] | Decarboxylase |
| 18287 | 2318 | PEROXIDASE PEROXIDASE (EC 1.11.1.7) PRECURSOR, CATIONIC (CLONEPNC2) - PEANUT, PIR2:B38265[PUTATIVE] | Oxidase |
| 18290 | 2319 | PEROXIDASE PEROXIDASE ATP13A - ARABIDOPSIS THALIANA, PID:E264765[PUTATIVE] | Oxidase |
| 18316 | 2320 | PHOSPHOFRUCTO-1-KINASE, PYROPHOSPHATE-DEPENDENT PHOSPHOFRUCTO-1-KINASE PYROPHOSPHATE-DEPENDENT PHOSPHOFRUCTO-1-KINASE, PRUNUS ARMENIACA, U93272 | Kinase |
| 18317 | 2321 | STEROID SULFOTRANSFERASE - LIKE PROTEIN STEROID SULFOTRANSFERASE, BRASSICA NAPUS, AF000307 | Transferases |
| 18322 | 2322 | SUBTILISIN PROTEASE - LIKE SUBTILISIN-LIKE PROTEASE, ARABIDOPSIS THALIANA, AF055848 | Protease |
| 18336 | 2323 | CALCIUM-DEPENDENT PROTEIN KINASE, ORYZA SATIVA, PIR2:S56652[PUTATIVE] | Kinase, Protein |
| 18343 | 2324 | RECEPTOR PROTEIN KINASE - LIKE PROTEIN CF-2.1, SOLANUM PIMPINELLIFOLIUM | Kinase, Protein |
| 18372 | 2325 | BETA-1,3-GLUCANASE BETA-1,3-GLUCANASE PRECURSOR - ORYZA SATIVA, PID:G4097948[PUTATIVE] | Glycosylase |
| 18379 | 2326 | GLUTAMINE AMIDOTRANSFERASE/CYCLASE | Cyclase |
| 18396 | 2327 | TRYPTOPHAN SYNTHASE BETA-SUBUNIT (TSB2) | Synthase |
| 18397 | 2328 | PROTEIN DISULFIDE-ISOMERASE (EC 5.3.4.1) ASPERGILLUS NIGER, PID:G899149[PUTATIVE] | Isomerase |
| 18414 | 2329 | DIHYDROKAEMPFEROL 4-REDUCTASE, MEDICAGO SATIVA, PIR2:S61416[PUTATIVE] | Reductase |
| 18418 | 2330 | RECEPTOR LIKE KINASE RECEPTOR-LIKE KINASE SFR2, BRASSICA OLERACEA, PID:E258943[PUTATIVE] | Kinase, Protein |
| 18419 | 2331 | RECEPTOR PROTEIN KINASE RECEPTOR PROTEIN KINASE, IPOMOEA TRIFIDA, PID:G836954[PUTATIVE] | Kinase, Protein |

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| 18433 | 2332 | PROTOCHLOROPHYLLIDE REDUCTASE PRECURSOR | Reductase |
| 18438 | 2333 | TRNA NUCLEOTIDYLTRANSFERASE METHANOBACTERIUM THERMOAUTOTROPHICUM,PID:G2621768[PUTATIVE] | - Transferases |
| 18445 | 2334 | UDP RHAMNOSE-ANTHOCYANIDIN-3-GLUCOSIDE RHAMNOSYLTRANSFERASE - LIKE PROTEIN UDP RHAMNOSE-ANTHOCYANIDIN-3-GLUCOSIDE RHAMNOSYLTRANSFERASE, PETUNIA HYBRIDA | Transferases |
| 18446 | 2335 | UDP RHAMNOSE-ANTHOCYANIDIN-3-GLUCOSIDE RHAMNOSYLTRANSFERASE - LIKE PROTEIN UDP RHAMNOSE-ANTHOCYANIDIN-3-GLUCOSIDE RHAMNOSYLTRANSFERASE, PETUNIA X HYBRIDA, PIR2:S36655 | Transferases |
| 18449 | 2336 | CARBOHYDRATE KINASE - LIKE PROTEIN PHOSPHOFRUCTOKINASE, BABESIA CANIS, AJ223322 | Kinase |
| 18468 | 2337 | PROTEIN PHOSPHATASE HOMOLOG (PPH1) | Phosphatase |
| 18482 | 2338 | PROTEIN KINASE LEPK7, LYCOPERSICON ESCULENTUM, GB:U89684[PUTATIVE] | Kinase, Protein |
| 18495 | 2339 | ATPASE, HAEMATOBIA IRRITANS, U12392[PUTATIVE] | ATPase |
| 18497 | 2340 | PECTINESTERASE LIKE PROTEIN PECTINESTERASE, LYCOPERSICON ESCULENTUM, Z94058 | Esterase |
| 18500 | 2341 | DIACYLGLYCEROL KINASE ZETA, HOMO SAPIENS, GB:U94905[PUTATIVE] | Kinase |
| 18501 | 2342 | DIACYLGLYCEROL KINASE (FRAGMENT) PUTATIVE DIACYLGLYCEROL KINASE - ARABIDOPSIS THALIANA, PID:G4454484[PUTATIVE] | Kinase |
| 18510 | 2343 | NADH DEHYDROGENASE NADH DEHYDROGENASE (UBIQUINONE) (EC 1.6.5.3) CHAIN NDII - YEAST, PIR2:S26704[PUTATIVE] | Dehydrogenase |
| 18520 | 2344 | (1-4)-BETA-MANNAN ENDOHYDROLASE MANNAN ENDO-1,4-BETA-MANNOSIDASE (EC 3.2.1.78) - TOMATO, PIR2:T04323[PUTATIVE] | Hydrolase |
| 18523 | 2345 | RECEPTOR PROTEIN KINASE LIKE PROTEIN LECTIN RECEPTOR-LIKE SERINE/THREONINE KINASE LECRK1, ARABIDOPSIS THALIANA, PIR2:S68589 | Kinase, Protein |

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| 18528 | 2346 | PROTEIN PHOSPHATASE 2C-LIKE PROTEIN PROTEIN PHOSPHATASE 2C-FISSION YEAST, PIR2:S54297 | Phosphatase |
| 18537 | 2347 | RECEPTOR-LIKE PROTEIN KINASE 5 PRECURSOR (RLK5) | Kinase, Protein |
| 18544 | 2348 | PROTEIN (FRAGMENT) PROTEIN KINASE XA21, ORYZA SATIVA, PIR1:A57676[PUTATIVE] | Kinase, Protein |
| 18553 | 2349 | RECEPTOR PROTEIN KINASE-LIKE PROTEIN RECEPTOR-LIKE PROTEIN KINASE 5, ARABIDOPSIS THALIANA, PIR1:S27756 | Kinase, Protein |
| 18555 | 2350 | SERINE/THREONINE KINASE-LIKE PROTEIN RECEPTOR-LIKE SERINE/THREONINE KINASE (RKF2), ARABIDOPSIS THALIANA, EMBL:AF024649 | Kinase, Protein |
| 18560 | 2351 | DIMETHYLANILINE MONOOXYGENASE (N-OXIDE- FORMING), SUS SCROFA DOMESTICA, PIR1:A33768[PUTATIVE] | Oxygenases |
| 18573 | 2352 | XYLOGLUCAN ENDOTRANSGLYCOSYLASE - LIKE PROTEIN XYLOGLUCAN ENDOTRANSGLYCOSYLASE 1,FAGUS SYLVATICA, PID:E1354157 | Glycosylase |
| 18593 | 2353 | SERINE/THREONINE-SPECIFIC KINASE LIKE PROTEIN SERINE/THREONINE-SPECIFIC KINASE LECRK1 - ARABIDOPSIS THALIANA, PIR2:S68589 | Kinase, Protein |
| 18597 | 2354 | RNA-DIRECTED DNA POLYMERASE - ARABIDOPSIS THALIANA RETROTRANSPOSON TA11-1, PIR2:S65812[PUTATIVE] | Polymerase |
| 18606 | 2355 | SERINE/THREONINE-SPECIFIC RECEPTOR PROTEIN KINASE SERINE/THREONINE-SPECIFIC RECEPTOR PROTEIN KINASE - ARABIDOPSIS THALIANA, PIR2:S71277[PUTATIVE] | Kinase, Protein |
| 18610 | 2356 | PHOSPHOFRUCTO-1-KINASE, PYROPHOSPHATE- DEPENDENT PHOSPHOFRUCTO-1-KINASE-LIKE PROTEIN PYROPHOSPHATE-DEPENDENT PHOSPHOFRUCTO-1-KINASE - PRUNUS ARMENIACA (APRICOT),PID:G2688822 | Kinase |
| 18614 | 2357 | ACID PHOSPHATASE-LIKE PROTEIN ACID PHOSPHATASE-1 (EC 3.1.3.-) - LYCOPERSICON ESCULENTUM,PIR2:T06587 | Phosphatase |

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| 18615 | 2358 | ACID PHOSPHATASE-LIKE PROTEIN ACID PHOSPHATASE-1 (EC 3.1.3.-) - LYCOPERSICON ESCULENTUM,PIR2:T06587 | Phosphatase |
| 18624 | 2359 | BETA-1,3-GLUCANASE-LIKE PROTEIN BETA-1,3- GLUCANASE (EC 3.2.1.-) 7 - GLYCINE MAX,PIR2:T05960 | Glycosylase |
| 18633 | 2360 | SERINE/THREONINE-SPECIFIC RECEPTOR PROTEIN KINASE-LIKE PROTEIN SERINE/THREONINE-SPECIFIC RECEPTOR PROTEIN KINASE LRRPK,PIR2:T08975 | Kinase, Protein |
| 18634 | 2361 | PHOSPHOLIPASE A2-LIKE PROTEIN PUTATIVE PHOSPHOLIPASE A2 - ORYZA SATIVA,PID:E1424908 | Lipase |
| 18635 | 2362 | PHOSPHOLIPASE A2 - ORYZA SATIVA,PID:E1424908[PUTATIVE] | Lipase |
| 18642 | 2363 | UDP-N-ACETYLGLUCOSAMINE O-ACYLTRANSFERASE - LIKE PROTEIN UDP-N-ACETYLGLUCOSAMINE O- ACYLTRANSFERASE, ALLOCHROMATIUM VINOSUM, GB:L76417 | Transferases |
| 18645 | 2364 | CYTIDINE DEAMINASE - LIKE PROTEIN CYTIDINE DEAMINASE 6, ARABIDOPSIS THALIANA, AF080676 | Deaminase |
| 18646 | 2365 | CYTIDINE DEAMINASE - LIKE PROTEIN CYTIDINE DEAMINASE 6, ARABIDOPSIS THALIANA, AF080676 | Deaminase |
| 18648 | 2366 | CYTIDINE DEAMINASE 7 | Deaminase |
| 18649 | 2367 | CYTIDINE DEAMINASE 6 (CDA6) | Deaminase |
| 18650 | 2368 | CYTIDINE DEAMINASE 2 (CDA2) | Deaminase |
| 18651 | 2369 | CYTIDINE DEAMINASE 3 (CDA3) | Deaminase |
| 18652 | 2370 | CYTIDINE DEAMINASE 5 (CDA5) | Deaminase |
| 18653 | 2371 | CYTIDINE DEAMINASE 4 (CDA4) | Deaminase |
| 18662 | 2372 | CYTOKININ OXIDASE - LIKE PROTEIN CYTOKININ OXIDASE, ZEA MAYS, GB:Y18377 | Oxidase |
| 18672 | 2373 | THREONINE SYNTHASE | Synthase |
| 18677 | 2374 | CHOLINE MONOOXYGENASE - LIKE PROTEIN CHOLINE MONOOXYGENASE PRECURSOR, SPINACIA OLERACEA,GB:U85780 | Oxygenases |
| 18687 | 2375 | SERINE/THREONINE-SPECIFIC RECEPTOR PROTEIN KINASE LRRPK | Kinase, Protein |

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| 18688 | 2376 | DIHYDROPTEROATE SYNTHASE-LIKE PROTEIN PROBABLE DIHYDROPTEROATE SYNTHASE - PISUM SATIVUM,PIR2:T06595 . | Synthase |
| 18705 | 2377 | PEROXIDASE ATP8A | Oxidase |
| 18715 | 2378 | XYLOGLUCAN ENDO-1,4-BETA-D-GLUCANASE PRECURSOR | Glycosylase |
| 18716 | 2379 | XYLOGLUCAN ENDO-1,4-BETA-D-GLUCANASE-LIKE PROTEIN XYLOGLUCAN ENDO-1,4-BETA-D- GLUCANASE (EC 3.2.1.-) XTR-3 - ARABIDOPSIS THALIANA,PIR2:S71222 | Glycosylase |
| 18717 | 2380 | XYLOGLUCAN ENDO-1,4-BETA-D-GLUCANASE-LIKE PROTEIN XYLOGLUCAN ENDO-1,4-BETA-D- GLUCANASE (EC 3.2.1.-) XTR-3 - ARABIDOPSIS THALIANA,PIR2:S71222 | Glycosylase |
| 18724 | 2381 | CYCLIC NUCLEOTIDE AND CALMODULIN-REGULATED ION CHANNEL-LIKE PROTEIN CYCLIC NUCLEOTIDE AND CALMODULIN-REGULATED ION CHANNEL - ARABIDOPSIS THALIANA,PID:E1421684 | Channel |
| 18732 | 2382 | NUCLEOTIDE SUGAR EPIMERASE-LIKE PROTEIN NUCLEOTIDE SUGAR EPIMERASE - VIBRIO VULNIFICUS,PID:G3093975 | Epimerase |
| 18735 | 2383 | CINNAMOYL-COA REDUCTASE - LIKE PROTEIN CINNAMOYL-COA REDUCTASE, SACCHARUM OFFICINARUM, GB:AJ231134 | Reductase |
| 18740 | 2384 | RECEPTOR-LIKE KINASE HOMOLOG SOMATIC EMBRYOGENESIS RECEPTOR-LIKE KINASE - DAUCUS CAROTA,PID:G2224911 | Kinase, Protein |
| 18741 | 2385 | ANILINE DIOXYGENASE (GMP SYNTHASE LIKE PROTEIN - ACINETOBACTER SP.,PID:D1013698[PUTATIVE] | Oxygenases |
| 18742 | 2386 | ANILINE DIOXYGENASE (GMP SYNTHASE LIKE PROTEIN - ACINETOBACTER SP.,PID:D1013698[PUTATIVE] | Oxygenases |
| 18743 | 2387 | ANILINE DIOXYGENASE (GMP SYNTHASE LIKE PROTEIN) - ACINETOBACTER SP.,PID:D1013698[PUTATIVE] | Oxygenases |

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| 18744 | 2388 | CYCLIC NUCLEOTIDE AND CALMODULIN-REGULATED ION CHANNEL-LIKE PROTEIN CYCLIC NUCLEOTIDE AND CALMODULIN-REGULATED ION CHANNEL - ARABIDOPSIS THALIANA, PID:E1421684 | Channel |
| 18746 | 2389 | 2-ACYLGLYCEROPHOSPHOETHANOLAMINE ACYLTRANSFERASE - AQUIFEX AEOLICUS, PIR2:E70476[PUTATIVE] | Transferases |
| 18783 | 2390 | OMEGA-6 FATTY ACID DESATURASE (FAD6) CHLOROPLAST | Desaturases |
| 18798 | 2391 | SERINE/THREONINE-SPECIFIC PROTEIN KINASE - LIKE SERINE/THREONINE-SPECIFIC PROTEIN KINASE PRO25, ARABIDOPSIS THALIANA, PIR2:A46373 | Kinase, Protein |
| 18799 | 2392 | WALL-ASSOCIATED KINASE 1, ARABIDOPSIS THALIANA, GB:AJ009696[PUTATIVE] | Kinase, Protein |
| 18802 | 2393 | 1,3-BETA-GLUCANASE - LIKE PROTEIN 1,3-BETA-GLUCANASE PRECURSOR, GOSSYPIMUM HIRSUTUM, PIR2:S72529 | Glycosylase |
| 18808 | 2394 | DNA TOPOISOMERASE LIKE- PROTEIN BACILLUS SUBTILIS DNA TOPOISOMERASE I; PID:G520753 | Isomerase |
| 18809 | 2395 | PROTEIN KINASE-LIKE PROTEIN SERINE/THREONINE-SPECIFIC PROTEIN KINASE, ARABIDOPSIS THALIANA, PIR2:S38326 | Kinase, Protein |
| 18810 | 2396 | RECEPTOR-LIKE KINASE, PETUNIA INFLATA, PATCHX:G1931655[PUTATIVE] | Kinase, Protein |
| 18812 | 2397 | RECEPTOR KINASE - LIKE PROTEIN RECEPTOR KINASE, PETUNIA INFLATA, PATCHX:G498278 | Kinase, Protein |
| 18816 | 2398 | CATION TRANSPORT PROTEIN CHAC, ESCHERICHIA COLI, PIR2:G64868, PREDICTED PROTEIN | Transporter |
| 18846 | 2399 | CELLULOSE SYNTHASE, AGROBACTERIUM TUMEFACIENS, PIR2:I39714[PUTATIVE] | Synthase |
| 18858 | 2400 | Glutamate KAINATE RECEPTOR, RATTUS NORVEGICUS, PIR2:I53474[PUTATIVE] | Receptor |
| 18863 | 2401 | PEROXIDASE - LIKE PROTEIN PEROXIDASE, SPINACIA OLERACEA, PID:G1781338 | Oxidase |

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| 18865 | 2402 | MONOGALACTOSYLDIACYLGLYCEROL SYNTHASE - LIKE PROTEIN MONOGALACTOSYLDIACYLGLYCEROL SYNTHASE, CUCUMIS SATIVUS, PID:G1805254 | Synthase |
| 18878 | 2403 | ANTHRANILATE HYDROXYCINNAMOYL/BENZOYLTRANSFERASE, DIAN THUS CARYOPHYLLUS, Z84384[PUTATIVE] | N-Transferases |
| 18887 | 2404 | SERINE/THREONINE PROTEIN KINASE LIKE PROTEIN VARIOUS PREDICTED PROTEIN KINASES, ARABIDOPSIS THALIANA | Kinase, Protein |
| 18912 | 2405 | MIXED-LINEAGE PROTEIN KINASE, HOMO SAPIENS, PIR:A53800[PUTATIVE] | Kinase, Protein |
| 18917 | 2406 | S-RECEPTOR KINASE -LIKE PROTEIN SERINE/THREONINE-SPECIFIC PROTEIN KINASE PK10 PRECURSOR, ORYZA SATIVA, PIR2:S50767 | Kinase, Protein |
| 18918 | 2407 | L-ASCORBATE PEROXIDASE - LIKE PROTEIN VARIOUS L-ASCORBATE PEROXIDASES | Oxidase |
| 18923 | 2408 | POLYGALACTURONASE (EC 3.2.1.15)PRECURSOR, LYCOPERSICON ESCULENTUM, PIR2:A25534[PUTATIVE] | Glycosylase |
| 18924 | 2409 | EXOPOLYGALACTURONASE, ARABIDOPSIS THALIANA, PIR2:S34200[PUTATIVE] | Glycosylase |
| 18927 | 2410 | CELLULOSE SYNTHASE CATALYTIC SUBUNIT (RSW1) | Synthase |
| 18940 | 2411 | DIMETHYLANILINE MONOOXYGENASE - LIKE PROTEIN DIMETHYLANILINE MONOOXYGENASE (N- OXIDE-FORMING), SUS SCROFA DOMESTICA, PIR:A33768 | Oxygenases |
| 18951 | 2412 | POTASSIUM CHANNEL PROTEIN ATKC POTASSIUM CHANNEL - SOLANUM TUBEROSUM, PATX:E264595 | Channel |
| 18957 | 2413 | PROTEIN KINASE PROTEIN KINASE TMK1, ARABIDOPSIS THALIANA, PIR1:JQ1674[PUTATIVE] | Kinase, Protein |
| 18970 | 2414 | PYROPHOSPHATE--FRUCTOSE-6-PHOSPHATE PHOSPHOTRANSFERASE PYROPHOSPHATE-- FRUCTOSE-6-PHOSPHATE 1-PHOSPHOTRANSFERASE (EC 2.7.1.90) - ENTAMOEBA HISTOLYTICA, PIR2:S68243[PUTATIVE] | 1-Transferases |

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| 18981 | 2415 | PROTEIN PHOSPHOPROTEIN PHOSPHATASE, ARABIDOPSIS THALIANA, PIR2:S55457[PUTATIVE] | Phosphatase |
| 18988 | 2416 | FE(II) TRANSPORT PROTEIN, ARABIDOPSIS THALIANA, GB:U27590[PUTATIVE] | Transporter |
| 18993 | 2417 | PYRUVATE DECARBOXYLASE-1 (PDC1) | Decarboxylase |
| 18997 | 2418 | CYCLOPROPANE-FATTY-ACYL-PHOSPHOLIPID SYNTHASE, ESCHERICHIA COLI, PIR2:A44292[PUTATIVE] | Synthase |
| 18998 | 2419 | CYCLOPROPANE-FATTY-ACYL-PHOSPHOLIPID SYNTHASE, ESCHERICHIA COLI, PIR2:A44292[PUTATIVE] | Synthase |
| 19008 | 2420 | PECTINESTERASE - LIKE PROTEIN PECTINESTERASE, PRUNUS PERSICA, X95991 | Esterase |
| 19009 | 2421 | PECTINESTERASE - LIKE PROTEIN PECTIN METHYLESTERASE-LIKE PROTEIN, ZEA MAYS, Y13285 | Esterase |
| 19019 | 2422 | GLYCOGENIN GLUCOSYLTRANSFERASE (EC 2.4.1.186) - HUMAN, PID:G1174167[PUTATIVE] | Transferases |
| 19022 | 2423 | DIHYDROKAEMPFEROL 4-REDUCTASE (EC 1.1.1.219) - SYNECHOCYSTIS, PIR2:S75325[PUTATIVE] | Reductase |
| 19028 | 2424 | PEROXIDASE ATP17A -LIKE PROTEIN PEROXIDASE ATP17A -A.THALIANA,PID:E252638 | Oxidase |
| 19029 | 2425 | SOMATIC EMBRYOGENESIS RECEPTOR-LIKE KINASE - LIKE PROTEIN SOMATIC EMBRYOGENESIS RECEPTOR- LIKE KINASE -DAUCUS CAROTA,PID:G2224911 | Kinase, Protein |
| 19030 | 2426 | POLYGALACTURONASE(EC 3.2.1.15) PRECURSOR - ERWINIA CAROTOVORA,PID:G42330[PUTATIVE] | Glycosylase |
| 19032 | 2427 | ABC-TYPE TRANSPORT PROTEIN SLL1623 - SYNECHOCYSTIS,PIR2:S74812[PUTATIVE] | Transporter |
| 19037 | 2428 | 2-DEHYDRO-3-DEOXYPHOSPHOHEPTONATE ALDOLASE | Aldolase |
| 19039 | 2429 | POTASSIUM TRANSPORTER ATKT5P (ATKT5) [PUTATIVE] | Transporter |
| 19044 | 2430 | CARBONATE DEHYDRATASE - LIKE PROTEIN CARBONATE DEHYDRATASE PRECURSOR, SPINACIA OLERACEA,PIR2:S28797 | Dehydratase |

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| 19054 | 2431 | AMINOTRANSFERASE (ASPC FAMILY), AQUIFEX AEOLICUS, PIR2:D70479[PUTATIVE] | Transferases |
| 19063 | 2432 | INOSITOL 1,3,4-TRISPHOSPHATE 5/6-KINASE, ARABIDOPSIS THALIANA, PIR2:JC5401[PUTATIVE] | Kinase |
| 19067 | 2433 | BETA-XYLAN ENDOHYDROLASE -LIKE PROTEIN (1,4)-BETA-XYLAN ENDOHYDROLASE ISOENZYME X-II, HORDEUM VULGARE, GB:U59313 | Hydrolase |
| 19068 | 2434 | (1,4)-BETA-XYLAN ENDOHYDROLASE, HORDEUM VULGARE, PID:G1718238[PUTATIVE] | Hydrolase |
| 19069 | 2435 | XYLAN ENDOHYDROLASE ISOENZYME X-I, HORDEUM VULGARE, PID:G1813595[PUTATIVE] | Hydrolase |
| 19070 | 2436 | XYLAN ENDOHYDROLASE ISOENZYME X-I, HORDEUM VULGARE, PID:G1813595[PUTATIVE] | Hydrolase |
| 19071 | 2437 | (1,4)-BETA-XYLAN ENDOHYDROLASE, ISOENZYME X-I, HORDEUM VULGARE, PID:G1718236[PUTATIVE] | Hydrolase |
| 19072 | 2438 | XYLAN ENDOHYDROLASE ISOENZYME X-I, HORDEUM VULGARE, PID:G1813595[PUTATIVE] | Hydrolase |
| 19073 | 2439 | PEROXIDASE PEROXIDASE ATP12A, ARABIDOPSIS THALIANA, PID:E264763[PUTATIVE] | Oxidase |
| 19077 | 2440 | PROLYL 4-HYDROXYLASE ALPHA(II)-SUBUNIT, MUSCULUS, PIR2:I49135[PUTATIVE] | Hydroxylase |
| 19078 | 2441 | PROTEIN PHOSPHATASE WIP1, HOMO SAPIENS, PID:G2218063[PUTATIVE] | Phosphatase |
| 19099 | 2442 | GLUCOSYLTRANSFERASE -LIKE PROTEIN IMMEDIATE-EARLY SALICYLATE-INDUCED GLUCOSYLTRANSFERASE, NICOTIANA TABACUM, PIR2:T03747 | Transferases |
| 19108 | 2443 | RECEPTOR PROTEIN KINASE - LIKE PROTEIN PROTEIN KINASE TMKL1, ARABIDOPSIS THALIANA, PID:E353150 | Kinase, Protein |
| 19109 | 2444 | CINNAMYL ALCOHOL DEHYDROGENASE - LIKE PROTEIN CINNAMYL ALCOHOL DEHYDROGENASE, POPULUS DELTOIDES, PATCHX:G288753 | Dehydrogenases |
| 19124 | 2445 | MYOSIN HEAVY CHAIN KINASE B, DICTYOSTELIUM DISCOIDEUM, U90946[PUTATIVE] | Kinase, Protein |

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| 19130 | 2446 | SERINE/THREONINE PROTEIN KINASE DAUCUS CAROTA SOMATIC EMBRYOGENESIS RECEPTOR-LIKE KINASE[PUTATIVE] | Kinase, Protein |
| 19136 | 2447 | SERINE/THREONINE PROTEIN KINASE DAUCUS CAROTA SOMATIC EMBRYOGENESIS RECEPTOR-LIKE KINASE, GB:U93048[PUTATIVE] | Kinase, Protein |
| 19137 | 2448 | FATTY ACID ELONGASE 1, KETOACYL-COA SYNTHASE, THALIANA,GB:U29142[PUTATIVE] | Synthase |
| 19140 | 2449 | ISOFLAVONE REDUCTASE - LIKE PROTEIN ISOFLAVONE REDUCTASE HOMOLOG P3, ARABIDOPSIS THALIANA, PIR2:S57613 | Reductase |
| 19157 | 2450 | ARGININE DECARBOXYLASE SPE2 | Decarboxylase |
| 19171 | 2451 | CHALCONE SYNTHASE - LIKE PROTEIN CHALCONE SYNTHASE HOMOLOG PRCHS1, PINUS RADIATA, GB:U90341 | Synthase |
| 19174 | 2452 | AMIDASE - LIKE PROTEIN AMIDASE, BACILLUS FIRMUS, GB:U64312 | Amidase |
| 19178 | 2453 | PHOSPHOLIPASE C, LISTERIA MONOCYTOGENES, PIR:A37204[PUTATIVE] | Lipase |
| 19179 | 2454 | PHOSPHATIDYL INOSITOL-SPECIFIC PHOSPHOLIPASE C, LISTERIA SEELIGERI, GB:X97014[PUTATIVE] | Lipase |
| 19186 | 2455 | L-ASCORBATE PEROXIDASE | Oxidase |
| 19187 | 2456 | BETA-GALACTOSIDASE - LIKE PROTEIN BETA-D- GALACTOSIDASE, MANGIFERA INDICA, PID:G2209358 | Glycosylase |
| 19189 | 2457 | PROTEIN KINASE - LIKE LEUCINE RICH REPEAT RECEPTOR-LIKE KINASE, ORYZA SATIVA, PATCHX:E267533 | Kinase, Protein |
| 19201 | 2458 | O-METHYLTRANSFERASE - LIKE PROTEIN CAFFEIC ACID O-METHYLTRANSFERASE, PINUS TAEDA, GB:U39301 | Transferases |
| 19202 | 2459 | O-METHYLTRANSFERASE - LIKE PROTEIN CAFFEIC ACID O-METHYLTRANSFERASE, PINUS TAEDA, GB:U39301 | Transferases |
| 19204 | 2460 | AMINO ACID PERMEASE - LIKE PROTEIN LILY MRNA, LILIUM LONGIFLORUM, GB:D21814 | Transporter |

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| 19209 | 2461 | PROTEIN KINASE APK1, ARABIDOPSIS THALIANA, PIR2:S28615[PUTATIVE] | Kinase, Protein |
| 19215 | 2462 | LIGAND-GATED ION CHANNEL PROTEIN, ARABIDOPSIS THALIANA (PREDICTED)[PUTATIVE] | Channel |
| 19216 | 2463 | SUGAR TRANSPORTER PROTEIN SUGAR TRANSPORTER, ARABIDOPSIS THALIANA, DB_XREF=PID:G1495273[PUTATIVE] | Transporter |
| 19228 | 2464 | DIHYDROFLAVONOL-4-REDUCTASE, GERBERA X SP., PIR2:S35189[PUTATIVE] | Reductase |
| 19231 | 2465 | THIOREDOXIN REDUCTASE (NADPH) 2 | Reductase |
| 19245 | 2466 | PROTEIN KINASE - LIKE PROTEIN SERINE/THREONINE-SPECIFIC PROTEIN KINASE APK1, ARABIDOPSIS THALIANA, PIR2:S28615 | Kinase, Protein |
| 19249 | 2467 | SERINE ACETYLTRANSFERASE, SERINE O-ACETYLTRANSFERASE, ARABIDOPSIS THALIANA, PIR2:S71207[PUTATIVE] | Transferases |
| 19252 | 2468 | POLYGALACTURONASE POLYGALACTURONASE 4, LYCOPERSICON ESCULENTUM, PID:G2459815[PUTATIVE] | Glycosylase |
| 19264 | 2469 | PHOSPHOLIPASE D, ARABIDOPSIS THALIANA, GB:U84568[PUTATIVE] | Lipase |
| 19266 | 2470 | PROLYL 4-HYDROXYLASE ALPHA (II) SUBUNIT, HOMO SAPIENS, GB:U90441[PUTATIVE] | Hydroxylase |
| 19267 | 2471 | PROCOLLAGEN-PROLINE DIOXYGENASE, CAENORHABDITIS ELEGANS, PIR2:A55069[PUTATIVE] | Oxygenases |
| 19282 | 2472 | ASCORBATE PEROXIDASE ASCORBATE PEROXIDASE, GOSSYPIUM HIRSUTUM, GB:U37060[PUTATIVE] | Oxidase |
| 19302 | 2473 | RECEPTOR PROTEIN KINASE CF-2.1 LEUCINE RICH REPEAT PROTEIN, SOLANUM PIMPINELLIFOLIUM, PATX:G1184075[PUTATIVE] | Kinase, Protein |
| 19322 | 2474 | PEROXIDASE LIKE PROTEIN | Oxidase |
| 19356 | 2475 | GLUCOSYLTRANSFERASE-LIKE PROTEIN | Transferases |
| 19360 | 2476 | GERANYLGERANYL PYROPHOSPHATE SYNTHASE | Synthase |
| 19368 | 2477 | UDP-GLUCURONYLTRANSFERASE-LIKE PROTEIN | Transferases |
| 19374 | 2478 | MAP3K-LIKE PROTEIN KINASE | Kinase, Protein |

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| 19394 | 2479 | HYDROXYNITRILE LYASE LIKE PROTEIN | Lyase |
| 19395 | 2480 | PECTINESTERASE LIKE PROTEIN | Esterase |
| 19404 | 2481 | RECEPTOR KINASE-LIKE PROTEIN | Kinase, Protein |
| 19428 | 2482 | RECEPTOR KINASE-LIKE PROTEIN | Kinase, Protein |
| 19431 | 2483 | BETA-KETOADIPATE ENOL-LACTONE HYDROLASE, ACINETOBACTER SP., L05770[PUTATIVE] | Hydrolase |
| 19438 | 2484 | PEROXIDASE, PRXR2 | Oxidase |
| 19440 | 2485 | PECTINESTERASE LIKE PROTEIN | Esterase |
| 19442 | 2486 | HYDROXYNITRILE LYASE LIKE PROTEIN | Lyase |
| 19445 | 2487 | FORMAMIDASE - LIKE PROTEIN FORMAMIDASE, METHYLOPHILUS METHYLOTROPHUS, PIR2:S74213 | Amidase |
| 19447 | 2488 | FORMAMIDASE - LIKE PROTEIN FORMAMIDASE, METHYLOPHILUS METHYLOTROPHUS, PIR2:S74213 | Amidase |
| 19452 | 2489 | N-ACETYLTRANSFERASE HOOKLESS 1 [PROBABLE] | Transferases |
| 19470 | 2490 | AMINO-ACID N-ACETYLTRANSFERASE, ESCHERICHIA COLI, PIR1:XYECAA[PUTATIVE] | Transferases |
| 19475 | 2491 | PHOSPHOENOLPYRUVATE CARBOXYKINASE (ATP) - LIKE PROTEIN | Kinase |
| 19478 | 2492 | AMMONIUM TRANSPORTER SAT1, GLYCINE MAX., AF069738[PUTATIVE] | Transporter |
| 19482 | 2493 | HEXOKINASE - LIKE PROTEIN HEXOKINASE, ARABIDOPSIS THALIANA, PIR2:S71205 | Kinase |
| 19486 | 2494 | ENDO-XYLOGLUCAN TRANSFERASE - LIKE PROTEIN ENDO-XYLOGLUCAN TRANSFERASE, GOSSYPIMUM HIRSUTUM, D88413 | Transferases |
| 19490 | 2495 | UDP-GLUCURONYLTRANSFERASE-LIKE PROTEIN | Transferases |
| 19507 | 2496 | CINNAMYL-ALCOHOL DEHYDROGENASE ELI3-1 | Dehydrogenases |
| 19508 | 2497 | CINNAMYL-ALCOHOL DEHYDROGENASE ELI3-2 | Dehydrogenases |
| 19528 | 2498 | CELLULOSE SYNTHASE - POPULUS ALBA X POPULUS TREMULA (CEL1),PID:G3511285[PUTATIVE] | Synthase |
| 19551 | 2499 | PECTINESTERASE PECTINESTERASE - LYCOPERSICON ESCULENTUM, PID:E312172[PUTATIVE] | Esterase |

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| 19554 | 2500 | GERANYLGERANYL PYROPHOSPHATE SYNTHASE-RELATED PROTEIN | Synthase |
| 19560 | 2501 | PROTEIN PHOSPHATASE-2C PROTEIN PHOSPHATASE-2C (PP2C) - MESEMBRYANTHEMUM CRYSTALLINUM, PID:G3608412[PUTATIVE] | Phosphatase |
| 19562 | 2502 | MONOOXYGENASE 2 (MO2) | Oxygenases |
| 19563 | 2503 | PHOSPHOLIPASE LIKE PROTEIN ARABIDOPSIS THALIANA PEARLI 4 MRNA, PID:G871782 | Lipase |
| 19564 | 2504 | PHOSPHOLIPASE LIKE PROTEIN ARABIDOPSIS THALIANA PEARLI 4 MRNA, PID:G871782 | Lipase |
| 19565 | 2505 | PHOSPHATIDYLINOSITOL SYNTHASE PHOSPHATIDYLINOSITOL SYNTHASE (PIS1) - ARABIDOPSIS THALIANA, PID:E1313354[PUTATIVE] | Synthase |
| 19567 | 2506 | GALACTOSIDASE LIKE PROTEIN SS-1,4-EXOGALACTANASE (BETA-GALACTOSIDASE) - LYCOPERSICON ESCULENTUM, PID:E1363850 | Glycosylase |
| 19577 | 2507 | PHOSPHOLIPASE C (EC 3.1.4.3) PRECURSOR, PHOSPHATIDYLINOSITOL-SPECIFIC - LISTERIA MONOCYTOGENES, PIR2:A37204[PUTATIVE] | Lipase |
| 19590 | 2508 | RECEPTOR-LIKE PROTEIN KINASE - LIKE PROTEIN RECEPTOR-LIKE PROTEIN KINASE RLK3, ARABIDOPSIS THALIANA, AJ011674 | Kinase, Protein |
| 19618 | 2509 | RECEPTOR-LIKE PROTEIN KINASE RECEPTOR-LIKE PROTEIN KINASE, CATHARANTHUS ROSEUS, Z73295[PUTATIVE] | Kinase, Protein |
| 19619 | 2510 | INOSITOL MONOPHOSPHATASE - LIKE PROTEIN MONO-PHOSPHATASE, STREPTOMYCES ANULATUS, X92429 | Phosphatase |
| 19628 | 2511 | GLUCOSE-1-PHOSPHATE ADENYLYLTRANSFERASE (APL3) | Transferases |
| 19630 | 2512 | NAD(P)H OXIDOREDUCTASE, ISOFLAVONE REDUCTASE - LIKE PROTEIN PYRC2, PYRUS COMMUNIS, AF071477 | Reductase |
| 19634 | 2513 | RECEPTOR PROTEIN KINASE - LIKE PROTEIN RECEPTOR PROTEIN KINASE ERECTA, ARABIDOPSIS THALIANA | Kinase, Protein |

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| 19639 | 2514 | CINNAMYL-ALCOHOL DEHYDROGENASE CAD1 | Dehydrogenases |
| 19641 | 2515 | CELLULOSE SYNTHASE CATALYTIC SUBUNIT (ATH-A) | Synthase |
| 19643 | 2516 | UBIQUITIN SPECIFIC PROTEASE 66 - GALLUS GALLUS,PID:G3800764[PUTATIVE] | Protease |
| 19652 | 2517 | MITOCHONDRIAL CARRIER - LIKE PROTEIN AGPET8, ASHBYA GOSSYPIL, EMBL:AJ006406 | Transporter |
| 19660 | 2518 | SHIKIMATE KINASE - LIKE PROTEIN SHIKIMATE KINASE PRECURSOR, LYCOPERSICON ESCULENTUM, GB:S21584 | Kinase |
| 19704 | 2519 | 2-DEHYDRO-3-DEOXYPHOSHOHEPTONATE ALDOLASE | Aldolase |
| 19722 | 2520 | PROTEIN - KINASE PROTEIN KINASE TMK1 (EC 2.7.1.-), RECEPTOR TYPE PRECURSOR, ARABIDOPSIS THALIANA, PIR:JQ1674[PUTATIVE] | Kinase, Protein |
| 19737 | 2521 | ANTHRANILATE N-BENZOYLTRANSFERASE - LIKE PROTEIN ANTHRANILATE N-BENZOYLTRANSFERASE, CLOVE PINK, PIR:T10717 | Transferases |
| 19740 | 2522 | LAX1 / AUX1 -LIKE PERMEASE | Transporter |
| 19741 | 2523 | ALPHA-1,4-N-ACETYLGLUCOSAMINYLTRANSFERASE, HOMO SAPIENS, EMBL:AF141315[PUTATIVE] | Transferases |
| 19742 | 2524 | ALPHA AMYLASE [PUTATIVE] | Glycosylase |
| 19743 | 2525 | PHOSPHATASE (CTDP1), HOMO SAPIENS, EMBL:AF154115; HYPOTHETICAL PROTEIN RNA POLYMERASE II CTD | Phosphatase |
| 19748 | 2526 | PYRUVATE DECARBOXYLASE-LIKE PROTEIN PYRUVATE DECARBOXYLASE (EC 4.1.1.1) PDC1 - ARABIDOPSIS THALIANA, PIR:T05315 | Decarboxylase |
| 19749 | 2527 | PYRUVATE DECARBOXYLASE-LIKE PROTEIN PYRUVATE DECARBOXYLASE (EC 4.1.1.1) PDC1 - ARABIDOPSIS THALIANA, PIR:T05315 | Decarboxylase |
| 19770 | 2528 | RECEPTOR LIKE PROTEIN KINASE RECEPTOR LIKE PROTEIN KINASE - ARABIDOPSIS THALIANA, EMBL:ATLECGENE | Kinase, Protein |
| 19771 | 2529 | RECEPTOR LIKE PROTEIN KINASE RECEPTOR LIKE PROTEIN KINASE - ARABIDOPSIS THALIANA, EMBL:ATLECGENE | Kinase, Protein |

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| 19772 | 2530 | RECEPTOR LIKE PROTEIN KINASE RECEPTOR LIKE PROTEIN KINASE - ARABIDOPSIS THALIANA, EMBL:ATLECGENE | Kinase, Protein |
| 19774 | 2531 | GAMMA-INTERFERON INDUCIBLE LYSOSOMAL THIOL REDUCTASE - HOMO SAPIENS,EMBL:AF097362[PUTATIVE] | Reductase |
| 19784 | 2532 | TRANSPORTER PROTEIN NA+/H+ ANTIPORTER PROTEINS[PUTATIVE] | Transporter |
| 19785 | 2533 | TRANSPORTER PROTEIN NA+/H+ ANTIPORTER PROTEINS[PUTATIVE] | Transporter |
| 19786 | 2534 | PROTEIN PHOSPHATASE TYPE 2C - SACCHAROMYCES CEREVISIAE, EMBL:U72346[PUTATIVE] | Phosphatase |
| 19808 | 2535 | PROTEIN KINASE - DIFFERENT SPECIES[PUTATIVE] | Kinase, Protein |
| 19809 | 2536 | (1-4)-BETA-MANNAN ENDOHYDROLASE-LIKE PROTEIN MANNAN ENDO-1,4-BETA-MANNOSIDASE (EC 3.2.1.78) - LYCOPERSICON ESCULENTUM, PIR:T04323 | Hydrolase |
| 19811 | 2537 | RECEPTOR PROTEIN KINASES[PUTATIVE] | Kinase, Protein |
| 19823 | 2538 | PROTEIN KINASE WALL-ASSOCIATED KINASE 2 WAK2 - ARABIDOPSIS THALIANA, EMBL:AJ012423[PUTATIVE] | Kinase, Protein |
| 19833 | 2539 | AMINO ACID TRANSPORT PROTEIN - ARABIDOPSIS THALIANA, EMBL:U39783[PUTATIVE] | Transporter |
| 19839 | 2540 | HYDROLASE AT2G32150 - ARABIDOPSIS THALIANA, EMBL:AC006223[PUTATIVE] | Hydrolase |
| 19841 | 2541 | RIBONUCLEASE II-LIKE PROTEIN RIBONUCLEASE II FAMILY PROTEIN, DEINOCOCCUS RADIODURANS, PIR:C75571 | Nuclease |
| 19843 | 2542 | ABC TRANSPORTER -LIKE PROTEIN NBD-LIKE PROTEIN POP, ARABIDOPSIS THALIANA, EMBL:AF127664 | Transporter |
| 19845 | 2543 | SERINE/THREONINE-SPECIFIC PROTEIN KINASE NAK | Kinase, Protein |
| 19846 | 2544 | UBIQUITIN-PROTEIN LIGASE E3-ALPHA -LIKE PROTEIN UBIQUITIN-PROTEIN LIGASE E3-ALPHA, MOUSE, PIR:T14318 | Ligase |
| 19856 | 2545 | PROTEIN PHOSPHATASE-2C, MESEMBRYANTHEMUM CRYSTALLINUM, EMBL:AF079355[PUTATIVE] | Phosphatase |

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| 19892 | 2546 | PROTEIN PHOSPHATASE - LIKE PROTEIN PROTEIN PHOSPHATASE 2C HOMOLOG, MESEMBRYANTHEMUM CRYSTALLINUM, EMBL:AF097667 | Phosphatase |
| 19896 | 2547 | PROTEIN KINASE - LIKE PROTEIN KINASE APK2A, ARABIDOPSIS THALIANA, EMBL:D88206 | Kinase, Protein |
| 19930 | 2548 | RECEPTOR LIKE PROTEIN KINASE RECEPTOR LIKE PROTEIN KINASE, ARABIDOPSIS THALIANA, EMBL:ATLECGENE | Kinase, Protein |
| 19943 | 2549 | LYSINE DECARBOXYLASE - LIKE PROTEIN LYSINE DECARBOXYLASE, EIKENELLA CORRODENS, EMBL:U89166 | Decarboxylase |
| 19979 | 2550 | MONODEHYDROASCORBATE REDUCTASE (NADH) - LIKE PROTEIN MONODEHYDROASCORBATE REDUCTASE (NADH), CUCUMBER, PIR:JU0182 | Reductase |
| 19986 | 2551 | S-RECEPTOR KINASE - LIKE PROTEIN S-RECEPTOR KINASE HOMOLOG PRECURSOR, RICE, PIR:S50767 | Kinase, Protein |
| 19990 | 2552 | HISTONE DEACETYLASE -LIKE PROTEIN HISTONE DEACETYLASE, HD2-P39, NUCLEOLAR, ZEA MAYS, PIR:T04141 | Esterase |
| 19992 | 2553 | BETA-(1-3)-GLUCOSYL TRANSFERASE, BRADYRHIZOBIIUM JAPONICUM, EMBL:AF047687[PUTATIVE] | Transferases |
| 19993 | 2554 | 3-DEOXY-D-MANNO-OCTULOSONIC ACID TRANSFERASE -LIKE PROTEIN 3-DEOXY-D-MANNO-OCTULOSONIC ACID TRANSFERASE, ESCHERICHIA COLI, PIR:JU0467 | Transferases |
| 20014 | 2555 | LIPASE -LIKE PROTEIN LIPASE ARAB-1, ARABIDOPSIS THALIANA, PIR:S68410 | Lipase |
| 20028 | 2556 | PHOSPHOGLYCERATE MUTASE - LIKE PROTEIN | Mutase |
| 20034 | 2557 | CARBONATE DEHYDRATASE - LIKE PROTEIN | Dehydratase |
| 20047 | 2558 | PECTATE LYASE-LIKE PROTEIN | Lyase |
| 20053 | 2559 | S-ADENOSYL-L-METHIONINE:SALICYLIC ACID CARBOXYL METHYLTRANSFERASE-LIKE PROTEIN | Transferases |
| 20054 | 2560 | S-ADENOSYL-L-METHIONINE:SALICYLIC ACID CARBOXYL METHYLTRANSFERASE-LIKE PROTEIN | Transferases |

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| 20068 | 2561 | 3-OXOACYL-[ACYL-CARRIER-PROTEIN] SYNTHASE - LIKE PROTEIN FABF 3-OXOACYL-[ACYL-CARRIER-PROTEIN]SYNTHASE .II, NEISSERIA MENINGITIDIS, EMBL:U73942 | Synthase |
| 20069 | 2562 | FATTY ACID ELONGASE - LIKE PROTEIN KCS1 FATTY ACID ELONGASE 3-KETOACYL-COA SYNTHASE 1, ARABIDOPSIS THALIANA, EMBL:AF053345 | Synthase |
| 20075 | 2563 | SULPHITE REDUCTASE | Reductase |
| 20110 | 2564 | NICOTIANAMINE SYNTHASE (DBJ BAA74589.1) | Synthase |
| 20111 | 2565 | PECTINESTERASE | Esterase |
| 20112 | 2566 | PECTINESTERASE | Esterase |
| 20132 | 2567 | CELLULOSE SYNTHASE CATALYTIC SUBUNIT (GB AAC39336.1) | Synthase |
| 20142 | 2568 | CHALCONE ISOMERASE, CHALCONE-FLAVONONE ISOMERASE [PUTATIVE] | Isomerase |
| 20147 | 2569 | MONOOXYGENASE | Oxygenases |
| 20149 | 2570 | PEROXIDASE | Oxidase |
| 20174 | 2571 | PHOSPHORIBOSYLANTHRANILATE ISOMERASE | Isomerase |
| 20175 | 2572 | LEUCOANTHOCYANIDIN DIOXYGENASE-LIKE PROTEIN | Oxygenases |
| 20178 | 2573 | CATIONIC AMINO ACID TRANSPORTER I[PUTATIVE] | Transporter |
| 20188 | 2574 | ANTHRANILATE SYNTHASE COMPONENT I-1 PRECURSOR (SP P32068) | Synthase |
| 20201 | 2575 | GLUCURONOSYL TRANSFERASE-LIKE PROTEIN | Transferases |
| 20202 | 2576 | GLUCURONOSYL TRANSFERASE-LIKE PROTEIN | Transferases |
| 20203 | 2577 | GLUCURONOSYL TRANSFERASE-LIKE PROTEIN | Transferases |
| 20204 | 2578 | GLUCURONOSYL TRANSFERASE-LIKE PROTEIN | Transferases |
| 20205 | 2579 | GLUCURONOSYL TRANSFERASE-LIKE PROTEIN | Transferases |
| 20231 | 2580 | SUCROSE TRANSPORTER PROTEIN | Transporter |
| 20244 | 2581 | LYSINE DECARBOXYLASE-LIKE PROTEIN | Decarboxylase |
| 20248 | 2582 | DIADENOSINE 5,5-P1,P4-TETRAPHOSPHATE HYDROLASE-LIKE PROTEIN | Hydrolase |
| 20286 | 2583 | PEROXIDASE (EMB CAA68212.1) | Oxidase |

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| 20287 | 2584 | PEROXIDASE | Oxidase |
| 20288 | 2585 | LECTIN-LIKE PROTEIN KINASE | Kinase, Protein |
| 20289 | 2586 | PROTEIN PHOSPHATASE 2C-LIKE | Phosphatase |
| 20296 | 2587 | RECEPTOR-LIKE PROTEIN KINASE | Kinase, Protein |
| 20299 | 2588 | ANTHRANILATE PHOSPHORIBOSYLTRANSFERASE-LIKE PROTEIN | Transferases |
| 20300 | 2589 | POLYGALACTURONASE INHIBITING PROTEIN 1; PGIP1 (GB AAF69827.1) | Glycosylase |
| 20301 | 2590 | POLYGALACTURONASE INHIBITING PROTEIN | Glycosylase |
| 20307 | 2591 | RECEPTOR PROTEIN KINASE-LIKE PROTEIN | Kinase, Protein |
| 20313 | 2592 | STEROID SULFOTRANSFERASE-LIKE PROTEIN | Transferases |
| 20314 | 2593 | STEROID SULFOTRANSFERASE-LIKE PROTEIN | Transferases |
| 20321 | 2594 | 10-DEACETYLBACCATIN III-10-O-ACETYLTRANSFERASE - TAXUS CUSPIDATA, AF193765, EMBL:AF193765[PUTATIVE] | Transferases |
| 20327 | 2595 | PROTEIN KINASE 6 - GLYCINE MAX, PIR:S29851[PUTATIVE] | Kinase, Protein |
| 20328 | 2596 | PROTEIN KINASE XA21 - ORYZA SATIVA, PIR:A57676[PUTATIVE] | Kinase, Protein |
| 20331 | 2597 | RECEPTOR-LIKE PROTEIN KINASE SEVERAL RECEPTOR-LIKE PROTEIN KINASES | Kinase, Protein |
| 20333 | 2598 | GIBBERELLIN 20-OXIDASE | Oxidase |
| 20341 | 2599 | RECEPTOR-LIKE PROTEIN KINASE-LIKE PROTEIN RECEPTOR-LIKE PROTEIN KINASE - IPOMOEA NIL (JAPANESE MORNING GLORY), PIR:T18536 | Kinase, Protein |
| 20349 | 2600 | AMIDASE [PUTATIVE] | AMIDASE |
| 20350 | 2601 | INOSITOL HEXAKISPHOSPHATE KINASE 2 - HOMO SAPIENS, EMBL:AF177145[PUTATIVE] | Kinase |
| 20354 | 2602 | PECTIN METHYL-ESTERASE-LIKE PROTEIN PECTIN METHYL-ESTERASE PER - MEDICAGO TRUNCATULA, EMBL:AJ249611 | Esterase |

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| 20355 | 2603 | PECTIN METHYL-ESTERASE-LIKE PROTEIN PECTIN METHYL-ESTERASE PER - MEDICAGO TRUNCATULA, EMBL:AJ249611 | Esterase |
| 20356 | 2604 | PECTIN METHYL-ESTERASE-LIKE PROTEIN PECTIN METHYL-ESTERASE PER - MEDICAGO TRUNCATULA, EMBL:AJ249611 | Esterase |
| 20361 | 2605 | 2-OXOGLUTARATE-DEPENDENT DIOXYGENASE SOLANUM CHACOENSE, EMBL:AF104925[PUTATIVE] | Oxygenases |
| 20375 | 2606 | RECEPTOR-LIKE PROTEIN KINASE[PUTATIVE] | Kinase, Protein |
| 20384 | 2607 | EXONUCLEASE-LIKE PROTEIN | Nuclease |
| 20385 | 2608 | ALPHA GALACTOSYLTRANSFERASE PROTEIN | Transferases |
| 20398 | 2609 | PROANTHRANILATE N-BENZOYLTRANSFERASE -LIKE PROTEIN ANTHRANILATE N-BENZOYLTRANSFERASE (EC 2.3.1.144), DIANTHUS CARYOPHYLLUS, PIR:T10717 | Transferases |
| 20399 | 2610 | N-HYDROXYCINNAMOYL/BENZOYLTRANSFERASE LIKE PROTEIN N-HYDROXYCINNAMOYL/BENZOYLTRANSFERASE, IPOMOEA BATATAS, EMBL:AB035183 | Transferases |
| 20400 | 2611 | N-HYDROXYCINNAMOYL/BENZOYLTRANSFERASE LIKE PROTEIN ANTHRANILATE N-BENZOYLTRANSFERASE, DIANTHUS CARYOPHYLLUS, PIR:T10717 | Transferases |
| 20416 | 2612 | GLYCEROPHOSPHODIESTER PHOSPHODIESTERASE LIKE PROTEIN GLYCEROPHOSPHODIESTER PHOSPHODIESTERASE, BORRELIA HERMSII, EMBL:BH40762 | Esterase |
| 20459 | 2613 | LIPASE/HYDROLASE GDSL-like -motif | Lipase |
| 20477 | 2614 | FLAVONOL SYNTHASE (FLS) (SP Q96330) | Synthase |
| 20480 | 2615 | AMINO ACID TRANSPORT PROTEIN AAP2 | Transporter |
| 20496 | 2616 | DNA-DIRECTED RNA POLYMERASE III CHAIN C53 SACCHAROMYCES CEREVISIAE, EMBL:X63501[PUTATIVE] | Polymerase |
| 20498 | 2617 | POTASSIUM TRANSPORT PROTEIN-LIKE SEVERAL POTASSIUM TRANSPORT PROTEINS | Transporter |

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| 20501 | 2618 | HYDROLASE ETBD1 - RHODOCOCBUS SP., EMBL:AB004320[PUTATIVE] | Hydrolase |
| 20528 | 2619 | BETA-GLUCOSIDASE - LIKE PROTEIN BETA- GLUCOSIDASE, GLYCINE MAX, AF000378 | Glycosylase |
| 20531 | 2620 | BETA-XYLOSIDASE - LIKE PROTEIN BETA- XYLOSIDASE, HYPOCREA JECORINA, EMBL:Z69257 | Glycosylase |
| 20534 | 2621 | PECTIN METHYLESTERASE - LIKE PROTEIN PECTIN METHYLESTERASE, MELANDRIUM ALBUM, EMBL:MAPME | Esterase |
| 20545 | 2622 | CELLULOSE SYNTHASE CATALYTIC SUBUNIT | Synthase |
| 20560 | 2623 | RECEPTOR PROTEIN KINASE -LIKE(FRAGMENT) RECEPTOR-LIKE PROTEIN KINASE ERECTA, ARABIDOPSIS THALIANA, EMBL:AC004484 | Kinase, Protein |
| 20563 | 2624 | 2,2-DIALKYLGLYCINE DECARBOXYLASE, P.CEPACIA, EMBL:PCDGD[PUTATIVE] | Decarboxylase |
| 20568 | 2625 | TREHALOSE-6-PHOSPHATE PHOSPHATASE -LIKE PROTEIN TREHALOSE-6-PHOSPHATE PHOSPHATASE, ARABIDOPSIS THALIANA, EMBL:AF007779 | Phosphatase |
| 20574 | 2626 | (3R)-HYDROXYMYRISTOYL-[ACYL CARRIER PROTEIN] DEHYDRATASE -LIKE PROTEIN BETA-HYDROXYACYL- ACP DEHYDRATASE PRECURSOR, TOXOPLASMA GONDII, EMBL:AF067150 | Dehydratase |
| 20577 | 2627 | CIS,CIS-MUCONATE TRANSPORT PROTEIN, ACINETOBACTER CALCOACETICUS, SWISSPROT:MUCK_ACICA[PUTATIVE] | Transporter |
| 20587 | 2628 | SERINE/THREONINE KINASE-LIKE PUTATIVE SERINE/THREONINE KINASE - SORGHUM BICOLOR, EMBL:Y14600 | Kinase, Protein |
| 20588 | 2629 | ALPHA-HYDROXYNITRILE LYASE-LIKE PROTEIN ALPHA-HYDROXYNITRILE LYASE HNL4 - MANIHOT ESCULENTA, EMBL:AJ223281 | Lyase |
| 20591 | 2630 | HISTIDINOL-PHOSPHATE AMINOTRANSFERASE-LIKE PROTEIN HISTIDINOL-PHOSPHATE AMINOTRANSFERASE - NICOTIANA TABACUM, EMBL:Y09204 | Transferases |

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| 20606 | 2631 | PROTEIN PHOSPHATASE PROTEIN TYROSINE PHOSPHATASE-LIKE PROTEIN PTPLB, MUS MUSCULUS, EMBL:AF169286[PUTATIVE] | Phosphatase |
| 20614 | 2632 | BETA-XYLOSIDASE - LIKE PROTEIN BETA- XYLOSIDASE, ASPERGILLUS NIDULANS, EMBL:ANXLND | Glycosylase |
| 20629 | 2633 | HISTIDINE KINASE - LIKE PROTEIN SENSORY TRANSDUCTION HISTIDINE KINASE SLR1759, SYNECHOCYSTIS SP., PIR:S75142 | Kinase, Protein |
| 20639 | 2634 | LIGNOSTILBENE-ALPHA,BETA-DIOXYGENASE GENE, SYNECHOCOCCUS PCC7942, EMBL:AF055873[PUTATIVE] | Oxygenases |
| 20644 | 2635 | CHORISMATE MUTASE CM2 | Mutase |
| 20659 | 2636 | SER/THR SPECIFIC PROTEIN KINASE-LIKE PROTEIN PROTEIN KINASE 1, POPULUS NIGRA, EMBL:AB041503 | Kinase, Protein |
| 20668 | 2637 | SUCROSE-PHOSPHATE SYNTHASE -LIKE PROTEIN SUCROSE-PHOSPHATE SYNTHASE ISOFORM 1, CITRUS UNSHIU, PIR:S72648 | Synthase |
| 20678 | 2638 | GLUTAMATE RECEPTOR GLUR3 LIGAND-GATED CHANNEL-LIKE PROTEIN PRECURSOR, ARABIDOPSIS THALIANA, EMBL:AF167355[PUTATIVE] | Channel |
| 20689 | 2639 | FLAVIN-CONTAINING MONOOXYGENASE, STREPTOMYCES COELICOLOR, PIR:T37052[PUTATIVE] | Oxygenases |
| 20690 | 2640 | SALICYLATE HYDROXYLASE, STREPTOMYCES COELICOLOR, PIR:T36193[PUTATIVE] | Hydroxylase |
| 20693 | 2641 | SERINE/THREONINE PROTEIN KINASE, ARABIDOPSIS THALIANA, SWISSPROT:NAK_ARATH[PUTATIVE] | Kinase, Protein |
| 20695 | 2642 | 1-D-DEOXYXYLULOSE 5-PHOSPHATE SYNTHASE - LIKE PROTEIN 1-D-DEOXYXYLULOSE 5-PHOSPHATE SYNTHASE, LYCOPERSICON ESCULENTUM, EMBL:AF143812 | Synthase |
| 20697 | 2643 | SERINE THREONINE TYROSINE-SPECIFIC PROTEIN KINASE APK1, ARABIDOPSIS THALIANA, PIR:S28615[PUTATIVE] | Kinase, Protein |
| 20711 | 2644 | L-GULONO-GAMMA-LACTONE OXIDASE, RATTUS NORVEGICUS, EMBL:RNFLAVIN[PUTATIVE] | Oxidase |

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| 20714 | 2645 | OLIGOPEPTIDE TRANSPORTER PROTEIN LEOPTI OLIGOPEPTIDE TRANSPORTER, LYCOPERSICON ESCULENTUM, EMBL:AF016713[PUTATIVE] | Transporter |
| 20719 | 2646 | MAP KINASE KINASE KINASE 1, MUS MUSCULUS, EMBL:AF117340[PUTATIVE] | Kinase, Protein |
| 20722 | 2647 | LYSOPHOSPHOLIPASE - LIKE PROTEIN LYSOPHOSPHOLIPASE HOMOLOG LPL1, ORYZA SATIVA, EMBL:AF039531 | Lipase |
| 20737 | 2648 | POTASSIUM TRANSPORT PROTEIN GLUTATHIONE- REGULATED POTASSIUM-EFFLUX SYSTEM PROTEIN KEFB, ESCHERICHIA COLI, SWISSPROT:P45522[PUTATIVE] | Transporter |
| 20745 | 2649 | DIAMINOPIMELATE DECARBOXYLASE - LIKE PROTEIN DIAMINOPIMELATE DECARBOXYLASE, ARABIDOPSIS THALIANA, EMBL:ATH249960 | Decarboxylase |
| 20748 | 2650 | ESTERASE - LIKE PROTEIN CINI PROTEIN - IMPORTED, BUTYRIVIBRIO FIBRISOLVENS, PIR:T44624[PUTATIVE] | Esterase |
| 20751 | 2651 | SUBTILISIN-LIKE PROTEASE - LIKE PROTEIN SUBTILISIN-LIKE PROTEASE, ARABIDOPSIS THALIANA, EMBL:AF098632 | Protease |
| 20752 | 2652 | LYSINE DECARBOXYLASE - LIKE PROTEIN LYSINE DECARBOXYLASE, EIKENELLA CORRODENS, EMBL:U89166 | Decarboxylase |
| 20766 | 2653 | NPK1-RELATED PROTEIN KINASE[PUTATIVE] | Kinase, Protein |
| 20770 | 2654 | TRANSMEMBRANE TRANSPORT PROTEIN[PUTATIVE] | Transporter |
| 20789 | 2655 | GLUCOSYLTRANSFERASE -LIKE PROTEIN GLUCOSYLTRANSFERASE ISSA, SALICYLATE- INDUCED, COMMON TOBACCO, PIR:T03747 | Transferases |
| 20797 | 2656 | ANTHRANILATE PHOSPHORIBOSYLTRANSFERASE - LIKE PROTEIN ANTHRANILATE PHOSPHORIBOSYLTRANSFERASE, GARDEN PEA, PIR:T06460 | Transferases |
| 20800 | 2657 | CALLOSE SYNTHASE CATALYTIC SUBUNIT -LIKE PROTEIN PUTATIVE CALLOSE SYNTHASE CATALYTIC SUBUNIT (CFL1), GOSSYPIMUM HIRSUTUM, EMBL:AF085717 | Synthase |

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| 20805 | 2658 | 5-FORMYLTETRAHYDROFOLATE CYCLO-LIGASE-LIKE PROTEIN 5-FORMYLTETRAHYDROFOLATE CYCLO- LIGASE (EC 6.3.3.2) - HOMO SAPIENS, EMBL:L38928 | Ligase |
| 20816 | 2659 | PROTEIN KINASE-LIKE PROTEIN KINASE 1 PNP1 - POPULUS NIGRA, EMBL:AB041503 | Kinase, Protein |
| 20828 | 2660 | ASPARTATE KINASE | Kinase |
| 20829 | 2661 | PROTEIN KINASE PRECURSOR - LIKE RECEPTOR-LIKE PROTEIN KINASE 5 PRECURSOR, ARABIDOPSIS THALIANA, SWISSPROT:RLK5_ARATH | Kinase, Protein |
| 20841 | 2662 | PEPTIDYL-PROLYL CIS-TRANS ISOMERASE, SPODOPTERA FRUGIPERDA, EMBL:SF15038[PUTATIVE] | Isomerase |
| 20842 | 2663 | TRANSALDOLASE - LIKE PROTEIN TRANSALDOLASE, SOLANUM TUBEROSUM, EMBL:U95923 | Aldolase |
| 20870 | 2664 | POLYAMINE OXIDASE | Oxidase |
| 20871 | 2665 | 24-STEROL C-METHYLTRANSFERASE | Transferases |
| 20874 | 2666 | TRANSPORTER-LIKE PROTEIN | Transporter |
| 20875 | 2667 | TRANSPORTER-LIKE PROTEIN | Transporter |
| 20887 | 2668 | ENDOXYLOGLUCAN TRANSFERASE (DBJ BAA81669.1) | Transferases |
| 20893 | 2669 | CHALCONE SYNTHASE (NARINGENIN-CHALCONE SYNTHASE) (TESTA 4 PROTEIN) (SP P13114) | Synthase |
| 20898 | 2670 | ALPHA-MANNOSIDASE | Glycosylase |
| 20906 | 2671 | ASPARTATE KINASE, LYSINE-SENSITIVE (GB AAB63104.1) | Kinase |
| 20910 | 2672 | ABC TRANSPORTER, ATP-BINDING PROTEIN[PUTATIVE] | Transporter |
| 20913 | 2673 | PEROXIDASE ATP20A (EMB CAA67338.1) | Oxidase |
| 20921 | 2674 | RECEPTOR PROTEIN KINASE-LIKE PROTEIN | Kinase, Protein |
| 20922 | 2675 | PROTOPORPHYRINOGEN IX OXIDASE | Oxidase |
| 20926 | 2676 | RIBULOSE-1,5-BISPHOSPHATE CARBOXYLASE/OXYGENASE SMALL SUBUNIT N- METHYLTRANSFERASE 1, SPINACIA OLERACEA CHLOROPLAST, PIR:T08996[PUTATIVE] | Transferases |
| 20927 | 2677 | KINASE - LIKE PROTEIN RING3 PROTEIN, HOMO SAPIENS, EMBL:X96670 | Kinase, Protein |

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| 20931 | 2678 | PROTEIN ESTERASE HDE, PETROLEUM-DEGRADING BACTERIUM HD-1, EMBL:AB029896[PUTATIVE] | Esterase |
| 20946 | 2679 | TRNA SYNTHASE - LIKE PROTEIN TRNA PSEUDOURIDINE SYNTHASE, FLAVOBACTERIUM JOHNSONIAE, EMBL:AF169967 | Synthase |
| 20948 | 2680 | N-ACETYLGLUCOSAMINYLTRANSFERASE III, MUS MUSCULUS, EMBL:MMU66844[PUTATIVE] | Transferases |
| 20957 | 2681 | HIGH AFFINITY NITRATE TRANSPORTER - LIKE PROTEIN HIGH AFFINITY NITRATE TRANSPORTER, ORYZA SATIVA, EMBL:AB008519 | Transporter |
| 20962 | 2682 | DNA METHYLTRANSFERASE 3, DANIO RERIO, EMBL:AF135438[PUTATIVE] | Transferases |
| 20965 | 2683 | POLYGALACTURONASE - LIKE PROTEIN POLYGALACTURONASE PG1, GLYCINE MAX, EMBL:AF128266 | Glycosylase |
| 20970 | 2684 | CINNAMOYL COA REDUCTASE - LIKE PROTEIN CINNAMOYL COA REDUCTASE, POPULUS TREMULOIDES, EMBL:AF217958 | Reductase |
| 20974 | 2685 | CARBONIC ANHYDRASE 2 | Anhydrase |
| 20978 | 2686 | FORMATE DEHYDROGENASE (FDH) | Dehydrogenases |
| 20986 | 2687 | GLUCOSYLTRANSFERASE -LIKE PROTEIN GLUCOSYLTRANSFERASE IS5A, COMMON TOBACCO, PIR:T03747 | Transferases |
| 20987 | 2688 | CYCLIC NUCLEOTIDE AND CALMODULIN-REGULATED ION CHANNEL -LIKE PROTEIN CYCLIC NUCLEOTIDE AND CALMODULIN-REGULATED ION CHANNEL CNGC6, ARABIDOPSIS THALIANA, EMBL:ATH17914 | Channel |
| 20988 | 2689 | CATION TRANSPORT PROTEIN PUTATIVE POTASSIUM TRANSPORTER ATKT2P, ARABIDOPSIS THALIANA, EMBL:AF012657[PUTATIVE] | Transporter |
| 20995 | 2690 | ALPHA-MANNOSIDASE -LIKE PROTEIN MANNOSYL-OLIGOSACCHARIDE 1,3-1,6-ALPHA-MANNOSIDASE, MOUSE, PIR:A41641 | Glycosylase |
| 20998 | 2691 | LYSOPHOSPHOLIPASE -LIKE PROTEIN LYSOPHOSPHOLIPASE HOMOLOG (HU-K5), HUMAN, EMBL:HSU67963 | Lipase |

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| 21008 | 2692 | SERINE/THREONINE SPECIFIC PROTEIN KINASE -LIKE SERINE/THREONINE/TYROSINE-SPECIFIC PROTEIN KINASE APK1, ARABIDOPSIS THALIANA, PIR:S28615 | Kinase, Protein |
| 21009 | 2693 | VOLTAGE-DEPENDENT ANION-SELECTIVE CHANNEL PROTEIN HSR2 | Channel |
| 21010 | 2694 | AUXIN TRANSPORT PROTEIN - LIKE AUXIN TRANSPORT PROTEIN (PIN7), ARABIDOPSIS THALIANA, EMBL:AF087820 | Transporter |
| 21011 | 2695 | PECTATE LYASE -LIKE PROTEIN PECTATE LYASE LAT59, TOMATO, PIR:S27098 | Lyase |
| 21018 | 2696 | PRX10 PEROXIDASE - LIKE PROTEIN PRX10 PEROXIDASE, SPINACIA OLERACEA, EMBL:SOY16776 | Oxidase |
| 21024 | 2697 | AMINO ACID TRANSPORT PROTEIN, ARABIDOPSIS THALIANA, EMBL:U39783[PUTATIVE] | Transporter |
| 21038 | 2698 | DNA METHYLTRANSFERASE 3, DANIO RERIO, EMBL:AF135438[PUTATIVE] | Transferases |
| 21039 | 2699 | RRNA METHYLASE - LIKE PROTEIN RRNA METHYLASE SPOU, AQUIFEX AEOLICUS, PIR:H70443 | Methylase |
| 21041 | 2700 | CYCLIC NUCLEOTIDE-GATED CATION CHANNEL | Channel |
| 21063 | 2701 | PHYTOCHELATIN SYNTHETASE PUTATIVE PHYTOCHELATIN SYNTHETASE - ARABIDOPSIS THALIANA, EMBL:AJ006787[PUTATIVE] | Synthase |
| 21064 | 2702 | MITOCHONDRIAL CARRIER PROTEIN MITOCHONDRIAL CARRIER PROTEIN - RIBES NIGRUM, EMBL:AJ007580[PUTATIVE] | Transporter |
| 21073 | 2703 | SERINE/THREONINE-SPECIFIC PROTEIN KINASE-LIKE PROTEIN SERINE/THREONINE-SPECIFIC PROTEIN KINASE NPK15 - NICOTIANA TABACUM | Kinase, Protein |
| 21086 | 2704 | CARBOXYLESTERASE-LIKE PROTEIN STEROL ESTERASE - RATTUS NORVEGICUS, EMBL:Z22803 | Esterase |
| 21087 | 2705 | BETA-GLUCAN-ELICITOR RECEPTOR - GLYCINE MAX, EMBL:D78510[PUTATIVE] | Receptor |
| 21094 | 2706 | PROTOCHLOROPHYLLIDE REDUCTASE HOMOLOG - ORYZA SATIVA, EMBL:AF093628[PUTATIVE] | Reductase |

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| 21100 | 2707 | RECEPTOR PROTEIN KINASE-LIKE PROTEIN PROBABLE SOMATIC EMBRYOGENESIS RECEPTOR- LIKE KINASE - DAUCUS CAROTA, EMBL:U93048 | Kinase, Protein |
| 21101 | 2708 | STEROID 5ALPHA-REDUCTASE-LIKE PROTEIN STEROID 5ALPHA-REDUCTASE - RATTUS NORVEGICUS, PIR:A34239 | Reductase |
| 21112 | 2709 | LIPASE-LIKE PROTEIN MONOGLYCERIDE LIPASE - MUS MUSCULUS, EMBL:AJ001118 | Lipase |
| 21119 | 2710 | CELLULOSE SYNTHASE CELA - RHIZOBIUM LEGUMINOSARUM, EMBL:AF121340[PUTATIVE] | Synthase |
| 21123 | 2711 | STEAROYL-ACYL CARRIER PROTEIN DESATURASE STEAROYL-ACYL CARRIER PROTEIN DESATURASE SAD1 - LINUM USITATISSIMUM, EMBL:AJ006957 | Desaturases |
| 21124 | 2712 | STEAROYL-ACYL CARRIER PROTEIN DESATURASE STEAROYL-ACYL CARRIER PROTEIN DESATURASE SAD1 - LINUM USITATISSIMUM, EMBL:AJ006957 | Desaturases |
| 21129 | 2713 | ACETOLACTATE SYNTHASE-LIKE PROTEIN | Synthase |
| 21139 | 2714 | ACETYL-COA CARBOXYLASE, BIOTIN CARBOXYL CARRIER PROTEIN OF ACETYL-COA CARBOXYLASE PRECURSOR (BCCP) (SP Q42533) | Carboxylase |
| 21141 | 2715 | N- HYDROXYCINNAMOYL/BENZOYLTRANSFERASE[PUTA TIVE] | Transferases |
| 21145 | 2716 | S-ADENOSYLMETHIONINE:2- DEMETHYLMENAQUINONE METHYLTRANSFERASE- LIKE PROTEIN | Transferases |
| 21148 | 2717 | TYROSINE PHOSPHATASE[PUTATIVE] | Phosphatase |
| 21150 | 2718 | PROTEIN KINASE-LIKE PROTEIN | Kinase, Protein |
| 21153 | 2719 | AUXIN TRANSPORT PROTEIN[PUTATIVE] | Transporter |
| 21159 | 2720 | RECEPTOR-LIKE PROTEIN KINASE | Kinase, Protein |
| 21169 | 2721 | CELLULASE (EC 3.2.1.4) PRECURSOR - XANTHOMONAS CAMPESTRIS PV. CAMPESTRIS, PIR:JH0158[PUTATIVE] | Cellulase |
| 21179 | 2722 | N-ACETLYTRANSFERASE F13E7.7 - ARABIDOPSIS THALIANA, EMBL:AC018363[PUTATIVE] | Transferases |

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| 21189 | 2723 | RECEPTOR PROTEIN KINASE -LIKE PROTEIN SERINE/THREONINE-SPECIFIC RECEPTOR PROTEIN KINASE (EC 2.7.1.-), ARABIDOPSIS THALIANA, PIR:S71277 | Kinase, Protein |
| 21190 | 2724 | CELLULOSE SYNTHASE CATALYTIC SUBUNIT -LIKE PROTEIN ATH-B, CELLULOSE SYNTHASE CATALYTIC SUBUNIT, ARABIDOPSIS THALIANA, EMBL:AF027174 | Synthase |
| 21200 | 2725 | SUGAR TRANSPORTER - LIKE PROTEIN D-XYLOSE- PROTON SYMPORTER (D-XYLOSE TRANSPORTER), LACTOBACILLUS BREVIS, SWISSPROT:XYLT_LACBR | Transporter |
| 21202 | 2726 | UDP GLUCOSE:FLAVONOID 3-O- GLUCOSYLTRANSFERASE -LIKE PROTEIN UDP GLUCOSE:FLAVONOID 3-O-GLUCOSYLTRANSFERASE, VITIS VINIFERA, EMBL:AF000372 | Transferases |
| 21203 | 2727 | UDP GLUCOSE:FLAVONOID 3-O- GLUCOSYLTRANSFERASE -LIKE PROTEIN UDP GLUCOSE:FLAVONOID 3-O-GLUCOSYLTRANSFERASE, VITIS VINIFERA, EMBL:AF000371 | Transferases |
| 21204 | 2728 | UDP GLUCOSE:FLAVONOID 3-O- GLUCOSYLTRANSFERASE -LIKE PROTEIN UDP GLUCOSE:FLAVONOID 3-O-GLUCOSYLTRANSFERASE, VITIS VINIFERA, EMBL:AF000372 | Transferases |
| 21219 | 2729 | POLYGALACTURONASE-LIKE PROTEIN | Glycosylase |
| 21221 | 2730 | GLUTATHIONE S-TRANSFERASE-LIKE PROTEIN | Transferases |
| 21222 | 2731 | PHYTOENE SYNTHASE (GB AAB65697.1) | Synthase |
| 21232 | 2732 | GLUTAMATE DECARBOXYLASE I (GAD I) (SP Q42521) | Decarboxylase |
| 21241 | 2733 | CELLULOSE SYNTHASE CATALYTIC SUBUNIT (IRX3) | Synthase |
| 21252 | 2734 | PHOSPHOGLUCOMUTASE-LIKE PROTEIN PHOSPHOGLUCOMUTASE, CHLOROPLAST - SPINACIA OLERACEA, EMBL:X75898 | Mutase |
| 21281 | 2735 | PEROXIDASE ATP13A | Oxidase |
| 21291 | 2736 | 5-METHYLTETRAHYDROPTEROYLTRIGLUTAMATE-- HOMOCYSTEINE S-METHYLTRANSFERASE | Transferases |
| 21297 | 2737 | PHOSPHORIBOSYLANTHRANILATE TRANSFERASE- LIKE PROTEIN | Transferases |

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| 21298 | 2738 | ANTHRANILATE PHOSPHORIBOSYLTRANSFERASE, CHLOROPLAST PRECURSOR (SP Q02166) | Transferases |
| 21311 | 2739 | PROTEIN DISULFIDE ISOMERASE-RELATED PROTEIN[PUTATIVE] | Isomerase |
| 21319 | 2740 | GALACTOSE-1-PHOSPHATE URIDYL TRANSFERASE-LIKE PROTEIN | Transferases |
| 21321 | 2741 | BETA-1,3-GLUCANASE-LIKE PROTEIN | Glycosylase |
| 21346 | 2742 | RECEPTOR KINASE PK3 PRECURSOR, MAIZE, PIR:T02753[PUTATIVE] | Kinase, Protein |
| 21349 | 2743 | SER/THR SPECIFIC PROTEIN KINASE - LIKE PROTEIN VARIOUS PROTEIN KINASE, ARABIDOPSIS THALIANA | Kinase, Protein |
| 21360 | 2744 | PROTEIN KINASE -LIKE PROTEIN PROTEIN KINASE 1, POPULUS NIGRA, EMBL:AB041503 | Kinase, Protein |
| 21365 | 2745 | PROTEIN 2'-HYDROXYISOFLAVONE REDUCTASE (EC 1.3.1.45) - NICOTIANA TABACUM, PIR:T02202[PUTATIVE] | Reductase |
| 21366 | 2746 | BETA-AMYLASE-LIKE PROTEIN BETA-AMYLASE - PRUNUS ARMENIACA, EMBL:AF139501 | Glycosylase |
| 21390 | 2747 | PROTEIN KINASE - LIKE PROTEIN PTO KINASE INTERACTOR 1 (PTI1), LYCOPERSICON ESCULENTUM, EMBL:SL28007 | Kinase, Protein |
| 21398 | 2748 | PECTIN METHYL ESTERASE -LIKE PROTEIN PECTIN METHYL ESTERASE, SOLANUM TUBEROSUM, EMBL:AF152172 | Esterase |
| 21403 | 2749 | TRNA ISOPENTENYLTRANSFERASE -LIKE PROTEIN TRNA ISOPENTENYLTRANSFERASE, SACCHAROMYCES CEREVISIAE, PIR:S67176 | Transferases |
| 21421 | 2750 | GLUCOSE-1-PHOSPHATE ADENYLYLTRANSFERASE (APL1/ADG2) | Transferases |
| 21427 | 2751 | PROTEIN PHOSPHATASE, KINASE ASSOCIATED | Phosphatase |
| 21428 | 2752 | PHOSPHOLIPASE - LIKE PROTEIN VARIOUS PREDICTED PHOSPHOLIPASE PROTEINS | Lipase |
| 21436 | 2753 | PEPTIDYL-PROLYL CIS-TRANS ISOMERASE - LIKE PROTEIN PEPTIDYL-PROLYL CIS-TRANS ISOMERASE A.THALIANA | Isomerase |

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| 21449 | 2754 | PERMEASE FAMILY PROTEIN TC0205, CHLAMYDIA MURIDARUM, PIR:D81729[PUTATIVE] | Transporter |
| 21457 | 2755 | GLYOXAL OXIDASE PRECURSOR, PHANEROCHAETE CHRYSOSPORIUM, PIR:A48296[PUTATIVE] | Oxidase |
| 21463 | 2756 | PEPTIDE TRANSPORT PROTEIN-LIKE PEPTIDE TRANSPORT PROTEIN - HORDEUM VULGARE, EMBL:AF023472 | Transporter |
| 21471 | 2757 | GLUTAMINE-TRNA LIGASE - LUPINUS LUTEUS, EMBL:X91787[PUTATIVE, PROTEIN C-TERMINUS OF] | Ligase |
| 21472 | 2758 | PECTIN METHYLESTERASE-LIKE PROTEIN PECTIN METHYL ESTERASE - SOLANUM TUBEROSUM, EMBL:AF152172 | Esterase |
| 21487 | 2759 | PEROXIDASE PEROXIDASE, LYCOPERSICON ESCULENTUM, PIR:S32768 | Oxidase |
| 21488 | 2760 | PEROXIDASE ATP N | Oxidase |
| 21503 | 2761 | IPP TRANSFERASE - LIKE PROTEIN TRNA DELTA(2)-ISOPENTENYLPYROPHOSPHATE TRANSFERASE (IPP TRANSFERASE), PSEUDOMONAS PUTIDA, EMBL:AF016312 | Transferases |
| 21504 | 2762 | RECEPTOR-LIKE PROTEIN KINASE - LIKE PROTEIN RECEPTOR-LIKE PROTEIN KINASE, ARABIDOPSIS THALIANA, EMBL:M84659 | Kinase, Protein |
| 21527 | 2763 | SUCROSE-PHOSPHATE SYNTHASE-LIKE PROTEIN SUCROSE-PHOSPHATE SYNTHASE (EC 2.4.1.14) ISOFORM 1 - CITRUS UNSHIU, EMBL:AB005023 | Synthase |
| 21532 | 2764 | BETA-1,3-GLUCANASE BG4 | Glycosylase |
| 21533 | 2765 | BETA-1,3-GLUCANASE BG5 | Glycosylase |
| 21538 | 2766 | BETA-1,3-GLUCANASE-LIKE PROTEIN BETA-1,3-GLUCANASE BG4 - A.THALIANA, EMBL:X79694 | Glycosylase |
| 21539 | 2767 | ETHYLENE-FORMING-ENZYME-LIKE DIOXYGENASE-LIKE PROTEIN ETHYLENE-FORMING-ENZYME-LIKE DIOXYGENASE - PRUNUS ARMENIACA, EMBL:U97530 | Oxygenases |
| 21540 | 2768 | MONOGALACTOSYLDIACYLGLYCEROL SYNTHASE | Synthase |
| 21547 | 2769 | RECEPTOR PROTEIN KINASE - LIKE PROTEIN KINASE XA21, ORYZA SATIVA, PIR:A57676 | Kinase, Protein |

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| 21554 | 2770 | ETHYLENE-FORMING-ENZYME-LIKE DIOXYGENASE - LIKE ETHYLENE-FORMING-ENZYME-LIKE DIOXYGENASE, PRUNUS ARMENIACA, EMBL:U97530 | Oxygenases |
| 21555 | 2771 | BETA-1,3-GLUCANASE - LIKE PROTEIN BETA-1,3-GLUCANASE BG4 AND BG5, A.THALIANA, EMBL:ATCBG45 | Glycosylase |
| 21568 | 2772 | RECEPTOR PROTEIN KINASE - LIKE RECEPTOR-LIKE PROTEIN KINASE PRK1, TOMATO, PIR:T07865 | Kinase, Protein |
| 21582 | 2773 | SUCROSE-UDP GLUCOSYLTRANSFERASE | Transferases |
| 21585 | 2774 | PECTINESTERASE - LIKE PROTEIN PROBABLE PECTINESTERASE PRECURSOR, GARDEN PEA, PIR:T06374 | Esterase |
| 21586 | 2775 | BETA-1,3-GLUCANASE - LIKE PROTEIN PROBABLE BETA-1,3-GLUCANASE, WHEAT, PIR:T06268 | Glycosylase |
| 21593 | 2776 | BETA-GLUCOSIDASE - LIKE PROTEIN BETA-GLUCOSIDASE, COMMON NASTURTIUM, PIR:T10521 | Glycosylase |
| 21594 | 2777 | BETA-D-GLUCAN EXOHYDROLASE - LIKE PROTEIN BETA-D-GLUCAN EXOHYDROLASE, NICOTIANA TABACUM, EMBL:AB017502 | Hydrolase |
| 21597 | 2778 | 5-METHYLTETRAHYDROPTEROYLTRIGLUTAMATE-HOMOCYSTEINE S-METHYLTRANSFERASE - LIKE PROTEIN 5-METHYLTETRAHYDROPTEROYLTRIGLUTAMATE-HOMOCYSTEINE S-METHYLTRANSFERASE, ARABIDOPSIS THALIANA, EMBL:U97200 | Transferases |
| 21605 | 2779 | HOMOSERINE DEHYDROGENASE-LIKE PROTEIN THRA BIFUNCTIONAL ENZYME - ESCHERICHIA COLI, PIR:B64720 | Dehydrogenases |
| 21634 | 2780 | PEROXIDASE ATP14A HOMOLOG | Oxidase |
| 21635 | 2781 | ACYL COA REDUCTASE-LIKE PROTEIN | Reductase |
| 21656 | 2782 | PREPHENATE DEHYDRATASE/CHORISMATE MUTASE-LIKE PROTEIN | Dehydratase |
| 21658 | 2783 | HISTONE DEACETYLASE-LIKE PROTEIN | Dehydratase |
| 21667 | 2784 | GLUCOSYLTRANSFERASE-LIKE PROTEIN | Transferases |
| 21673 | 2785 | LIPASE/HYDROLASE GDSL-like -motif | Lipase |

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| 21677 | 2786 | PROTEASE-LIKE PROTEIN | Protease |
| 21682 | 2787 | NA ⁺ /H ⁺ ANTIporter-LIKE PROTEIN | Transporter |
| 21683 | 2788 | NA ⁺ /H ⁺ ANTIporter-LIKE PROTEIN | Transporter |
| 21688 | 2789 | SERINE CARBOXYPEPTIDASE[PUTATIVE] | Protease |
| 21693 | 2790 | 2-ISOPROPYLMALATE SYNTHASE-LIKE; HOMOCITRATE SYNTHASE-LIKE | Synthase |
| 21694 | 2791 | 2-ISOPROPYLMALATE SYNTHASE-LIKE PROTEIN | Synthase |
| 21709 | 2792 | SERINE/THREONINE PROTEIN KINASE-LIKE PROTEIN | Kinase, Protein |
| 21736 | 2793 | FERREDOXIN-THIOREDOXIN REDUCTASE VARIABLE CHAIN[PUTATIVE] | Reductase |
| 21751 | 2794 | PHOSPHOTRANSFERASE[PUTATIVE] | Transferases |
| 21759 | 2795 | POLYA POLYMERASE[PUTATIVE] | Polymerase |
| 21769 | 2796 | GALACTINOL SYNTHASE | Synthase |
| 21771 | 2797 | AMINO ACID TRANSPORTER | Transporter |
| 21776 | 2798 | PECTINACETYLESTERASE | Esterase |
| 21783 | 2799 | ACYLTRANSFERASE | Transferases |
| 21785 | 2800 | DELTA-(+)CADINENE SYNTHASE (D-CADINENE SYNTHASE) | Synthase |
| 21790 | 2801 | RECEPTOR-PROTEIN KINASE-LIKE PROTEIN | Kinase, Protein |
| 21796 | 2802 | PEROXIDASE-LIKE PROTEIN | Oxidase |
| 21797 | 2803 | RECEPTOR-LIKE PROTEIN KINASE | Kinase, Protein |
| 21798 | 2804 | ENDOCHITINASE ACIDIC (DBJ BAA21861.1) | Chitinase |
| 21799 | 2805 | RECEPTOR-LIKE PROTEIN KINASE | Kinase, Protein |
| 21819 | 2806 | STARCH SYNTHASE SOLUBLE | Synthase |
| 21842 | 2807 | FLAVANONE 3-HYDROXYLASE-LIKE PROTEIN | Hydroxylase |
| 21945 | 2808 | FLAVIN-CONTAINING MONOOXYGENASE, RHESUS MACAQUE, SWISSPROT:FMO2_MACMU[PUTATIVE] | Oxygenases |
| 21966 | 2809 | RECEPTOR-LIKE PROTEIN KINASE - LIKE RECEPTOR- LIKE PROTEIN KINASE 5, ARABIDOPSIS THALIANA, PIR:S27756 | Kinase, Protein |
| 21974 | 2810 | PROTEIN PHOSPHATASE - LIKE PROTEIN PHOSPHATASE-2C, MESEMBRYANTHEMUM CRYSTALLINUM, AF075579 | Phosphatase |

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| 21987 | 2811 | LYSINE DECARBOXYLASE, ARABIDOPSIS THALIANA[PUTATIVE] | Decarboxylase |
| 22004 | 2812 | UTP-GLUCOSE GLUCOSYLTRANSFERASE - LIKE PROTEIN UTP-GLUCOSE GLUCOSYLTRANSFERASE, CASSAVA, PIR:S41951 | Transferases |
| 22010 | 2813 | PYRUVATE WATER DIKINASE, ARCHAEoglobus FULGIDUS, PIR:F69338[PUTATIVE] | Kinase |
| 22013 | 2814 | ISOPENICILLIN N EPIMERASE, STREPTOMYCES CLAVULIGERUS, EMBL:M32324[PUTATIVE] | Epimerase |
| 22020 | 2815 | PECTINACETYLESTERASE PRECURSOR - LIKE PROTEIN PECTINACETYLESTERASE PRECURSOR, VIGNA RADIATA, PIR:S68805 | Esterase |
| 22034 | 2816 | PECTINESTERASE 2 PRECURSOR, ARABIDOPSIS THALIANA, PIR:PC4168[PUTATIVE] | Esterase |
| 22035 | 2817 | FERROPORTIN1, MUS MUSCULUS, EMBL:AF226613[PUTATIVE] | Transporter |
| 22041 | 2818 | RRNA METHYLASES[PUTATIVE] | Methylase |
| 22047 | 2819 | DNA POLYMERASE SUBUNIT [PUTATIVE] | Polymerase |
| 22063 | 2820 | ION CHANNEL - LIKE PROTEIN LIGAND GATED CHANNEL-LIKE PROTEIN, BRASSICA NAPUS, EMBL:AF109392 | Channel |
| 22074 | 2821 | G protein SEVEN TRANSMEMBRANE DOMAIN ORPHAN RECEPTOR, MUS MUSCULUS, EMBL:AF051098[PUTATIVE] | Receptor |
| 22094 | 2822 | AMINO ACID AMINOTRANSFERASE BRANCHED-CHAIN AMINO ACID AMINOTRANSFERASE - PSEUDOMONAS AERUGINOSA, SWISSPROT:ILVE_PSEAE[PUTATIVE] | Transferases |
| 22096 | 2823 | SIGNAL PEPTIDASE | Protease |
| 22104 | 2824 | PROTEIN KINASE-LIKE PROTEIN MAP3KA MEK KINASE - ARABIDOPSIS THALIANA, EMBL:U58918 | Kinase, Protein |
| 22106 | 2825 | POLYGALACTURONASE-LIKE PROTEIN POLYGALACTURONASE - LYCOPERSICON ESCULENTUM, EMBL:AF118567 | Glycosylase |
| 22132 | 2826 | PROTEIN KINASE - LIKE PROTEIN MEKK5 (ASK1, MAPKKK5) GENE FOR MAP/ERK KINASE KINASE 5, HOMO SAPIENS, TREMBL:HS325F22 | Kinase, Protein |

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| 22140 | 2827 | PECTIN METHYL-ESTERASE - LIKE PROTEIN PECTIN METHYL-ESTERASE PER, MEDICAGO TRUNCATULA, EMBL:MTR249611 | Esterase |
| 22146 | 2828 | PROTEIN PHOSPHATASE - LIKE PROTEIN PHOSPHATASE-2C, MESEMBRYANTHEMUM CRYSTALLINUM, EMBL:AF075581 | Phosphatase |
| 22189 | 2829 | 1-AMINOCYCLOPROPANE-1-CARBOXYLATE SYNTHASE 1-AMINOCYCLOPROPANE-1-CARBOXYLATE SYNTHASE - ARABIDOPSIS THALIANA, EMBL:U26542, FRAGMENT OF | Synthase |
| 22221 | 2830 | RECEPTOR-LIKE PROTEIN KINASE PRECURSOR - LIKE RECEPTOR-LIKE PROTEIN KINASE, MADAGASCAR PERIWINKLE, PIR:T10060 | Kinase, Protein |
| 22268 | 2831 | GALACTINOL SYNTHASE - LIKE | Synthase |
| 22340 | 2832 | ADENYLATE KINASE -LIKE PROTEIN PREDICTED PROTEINS, ARABIDOPSIS THALIANA | Kinase |
| 22388 | 2833 | RECEPTOR-LIKE PROTEIN KINASE - LIKE PROTEIN RECEPTOR-LIKE PROTEIN KINASE, ARABIDOPSIS THALIANA, EMBL:ATRLPKB | Kinase, Protein |
| 22390 | 2834 | RECEPTOR-LIKE PROTEIN KINASE RECEPTOR-LIKE PROTEIN KINASE PRK1, LYCOPERSICON ESCULENTUM, PIR:T07865[PUTATIVE] | Kinase, Protein |
| 22424 | 2835 | BETA-1,3-GLUCANASE[PUTATIVE] | Glycosylase |
| 22425 | 2836 | HISTIDINE KINASE-LIKE PROTEIN | Kinase, Protein |
| 22446 | 2837 | SERINE/THREONINE PROTEIN KINASE-LIKE | Kinase, Protein |
| 22475 | 2838 | PROTEIN PHOSPHATASE-2C PP2C-LIKE | Phosphatase |
| 22476 | 2839 | ASPARTYL PROTEASE-LIKE | Protease |
| 22477 | 2840 | GSH-DEPENDENT DEHYDROASCORBATE REDUCTASE 1-LIKE | Reductase |
| 22502 | 2841 | GLUCAN SYNTHASE GLUCAN SYNTHASES - DIFFERENT SPECIES[PUTATIVE] | Synthase |
| 22521 | 2842 | TRANSPORTER PROTEIN NA ⁺ /H ⁺ -EXCHANGING PROTEIN NAPA - ENTEROCOCCUS HIRAE, PIR:A42111[PUTATIVE] | Transporter |

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| 22532 | 2843 | CAFFEIC ACID O-METHYLTRANSFERASE-LIKE PROTEIN LIGNIN-BISPECIFIC O- METHYLTRANSFERASE - POPULUS TREMULOIDES, EMBL:X62096 | Transferases |
| 22533 | 2844 | SUCROSE SYNTHASE-LIKE PROTEIN SUCROSE SYNTHASE - CITRUS UNSHIU, EMBL:AB022091 | Synthase |
| 22560 | 2845 | RECEPTOR PROTEIN KINASE-LIKE PROTEIN | Kinase, Protein |
| 22594 | 2846 | PROTEIN KINASE - LIKE PROTEIN PTO KINASE INTERACTOR 1 (PTI1), LYCOPERSICON ESCULENTUM, EMBL:SL28007 | Kinase, Protein |
| 22610 | 2847 | GLUCURONOSYL TRANSFERASE-LIKE PROTEIN GLUCURONOSYL TRANSFERASE-LIKE PROTEIN, TOMATO, PIR:S39507 | Transferases |
| 22611 | 2848 | QUINONE OXIDOREDUCTASE (EC 1.6.5.5) P1, ARABIDOPSIS THALIANA, PIR:S57611[PUTATIVE] | Reductase |
| 22616 | 2849 | GLUCOSYLTRANSFERASE-LIKE PROTEIN UDP- GLUCOSE GLUCOSYLTRANSFERASE - SORGHUM BICOLOR, EMBL:AF199453 | Transferases |
| 22617 | 2850 | SAMT-LIKE PROTEIN S-ADENOSYL-L- METHIONINE:SALICYLIC ACID CARBOXYL METHYLTRANSFERASE (SAMT)- CLARKIA BREWERI, EMBL:AF133053 | Transferases |
| 22619 | 2851 | GLUCOSYLTRANSFERASE-LIKE PROTEIN UDP- GLUCOSE GLUCOSYLTRANSFERASE - SORGHUM BICOLOR, EMBL:AF199453 | Transferases |
| 22628 | 2852 | ANTHRANILATE N-BENZOYLTRANSFERASE -LIKE PROTEIN ANTHRANILATE N-BENZOYLTRANSFERASE (EC 2.3.1.144), CLOVE PINK, PIR:T10717 | Transferases |
| 22636 | 2853 | WALL-ASSOCIATED KINASE 4 (WAK4), ARABIDOPSIS THALIANA, EMBL:ATH9695 | Kinase, Protein |
| 22639 | 2854 | RECEPTOR SERINE/THREONINE PROTEIN KINASE - LIKE RECEPTOR SERINE/THREONINE KINASE PR5K, ARABIDOPSIS THALIANA, EMBL:AT48698 | Kinase, Protein |
| 22640 | 2855 | RECEPTOR SERINE/THREONINE PROTEIN KINASE - LIKE RECEPTOR SERINE/THREONINE KINASE PR5K, ARABIDOPSIS THALIANA, EMBL:AT48698 | Kinase, Protein |

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| 22641 | 2856 | RECEPTOR SERINE/THREONINE PROTEIN KINASE - LIKE RECEPTOR SERINE/THREONINE KINASE PR5K, ARABIDOPSIS THALIANA, EMBL:AT48698 | Kinase, Protein |
| 22656 | 2857 | RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR (RUBISCO SMALL SUBUNIT 3B) (SP P10798) | Carboxylase |
| 22657 | 2858 | RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 2B PRECURSOR (RUBISCO SMALL SUBUNIT 2B) (SP P10797) | Carboxylase |
| 22658 | 2859 | RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1B PRECURSOR (RUBISCO SMALL SUBUNIT 1B) (SP P10796) | Carboxylase |
| 22668 | 2860 | TRYPTOPHAN SYNTHASE BETA CHAIN | Synthase |
| 22671 | 2861 | PROTEIN KINASE[PUTATIVE] | Kinase, Protein |
| 22697 | 2862 | TRANSPORTER -LIKE PROTEIN N SYSTEM AMINO ACIDS TRANSPORTER NAT-1, MUS MUSCULUS, EMBL:AF159856 | Transporter |
| 22717 | 2863 | RECEPTOR PROTEIN KINASE - LIKE PROTEIN RECEPTOR-PROTEIN KINASE-LIKE PROTEIN, ARABIDOPSIS THALIANA, PIR:T45786 | Kinase, Protein |
| 22718 | 2864 | RECEPTOR PROTEIN KINASE - LIKE PROTEIN RECEPTOR SERINE/THREONINE KINASE PR5K, ARABIDOPSIS THALIANA, EMBL:AT48698 | Kinase, Protein |
| 22720 | 2865 | ACYLTRANSFERASE - LIKE PROTEIN ANTHOCYANIN 5-AROMATIC ACYLTRANSFERASE, GENTIANA TRIFLORA, EMBL:AB010708 | Transferases |
| 22723 | 2866 | ACYLTRANSFERASE -LIKE PROTEIN ANTHOCYANIN 5-AROMATIC ACYLTRANSFERASE, GENTIANA TRIFLORA, EMBL:AB010708 | Transferases |
| 22724 | 2867 | ACYLTRANSFERASE -LIKE PROTEIN ANTHOCYANIN ACYLTRANSFERASE, PERILLA FRUTESCENS, EMBL:AB029340 | Transferases |
| 22754 | 2868 | RECEPTOR PROTEIN KINASE -LIKE PROTEIN PROTEIN KINASE XA21, RJCE, PIR:A57676 | Kinase, Protein |
| 22773 | 2869 | PEROXIDASE ATP24A | Oxidase |

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| 22798 | 2870 | DEGP PROTEASE-LIKE PROTEIN DEGP PROTEASE PRECURSOR - ARABIDOPSIS THALIANA, EMBL:AF028842 | Protease |
| 22806 | 2871 | POLYGALACTURONASE-LIKE PROTEIN POLYGALACTURONASE PRECURSOR - LYCOPERSICON ESCULENTUM, PIR:S57806 | Glycosylase |
| 22830 | 2872 | PEROXIDASE ATP26A | Oxidase |
| 22835 | 2873 | PROTEASE SERINE PROTEINASE DO, BACILLUS SUBTILIS, PIR:A69643[PUTATIVE] | Protease |
| 22853 | 2874 | RECEPTOR-LIKE PROTEIN KINASE RECEPTOR-LIKE SERINE/THREONINE KINASE RKF2, ARABIDOPSIS THALIANA, EMBL:AF024649 | Kinase, Protein |
| 22854 | 2875 | RAFFINOSE SYNTHASE -LIKE PROTEIN RAFFINOSE SYNTHASE RFS, CUCUMIS SATIVUS, EMBL:AF073744 | Synthase |
| 22893 | 2876 | AMINO ACID PERMEASE | Transporter |
| 22900 | 2877 | UROPHORPHYRIN III METHYLASE (GB AAB92676.1) | Methylase |
| 22914 | 2878 | LIPASE/HYDROLASE GDSL-like -motif | Lipase |
| 22919 | 2879 | N-HYDROXYCINNAMOYL/BENZOYLTRANSFERASE- LIKE PROTEIN | Transferases |
| 22931 | 2880 | PURINE PERMEASE-LIKE PROTEIN | Transporter |
| 22933 | 2881 | RECEPTOR KINASE-LIKE PROTEIN | Kinase, Protein |
| 22937 | 2882 | GLUTATHIONE TRANSFERASE-LIKE | Transferases |
| 22939 | 2883 | GLUTATHIONE TRANSFERASE | Transferases |
| 22941 | 2884 | PROTEIN KINASE-LIKE | Kinase, Protein |
| 22962 | 2885 | FOLYLPOLYGLUTAMATE SYNTHASE-LIKE PROTEIN | Synthase |
| 22975 | 2886 | NA ⁺ /H ⁺ ANTIporter-LIKE PROTEIN | Transporter |
| 22990 | 2887 | CMP-SIALIC ACID TRANSPORTER-LIKE PROTEIN | Transporter |
| 22994 | 2888 | AMINO ACID PERMEASE-LIKE PROTEIN; PROLINE TRANSPORTER-LIKE PROTEIN | Transporter |
| 23001 | 2889 | POLYGALACTURONASE-LIKE PROTEIN | Glycosylase |
| 23003 | 2890 | LIPASE/HYDROLASE GDSL-like -motif | Lipase |
| 23024 | 2891 | BETA-1,3-GLUCANASE-LIKE PROTEIN | Glycosylase |
| 23026 | 2892 | RECEPTOR LECTIN KINASE-LIKE PROTEIN | Kinase, Protein |
| 23031 | 2893 | LIPASE/HYDROLASE GDSL-like -motif | Lipase |

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| 23032 | 2894 | PEROXIDASE (EMB CAA66960.1) | Oxidase |
| 23035 | 2895 | TETRACYCLINE TRANSPORTER PROTEIN[PUTATIVE] | Transporter |
| 23058 | 2896 | SERINE/THREONINE PROTEIN KINASE-LIKE PROTEIN | Kinase, Protein |
| 23079 | 2897 | ALLENE OXIDE SYNTHASE (EMB CAA73184.1) | Synthase |
| 23086 | 2898 | BETA-1,3-GLUCANASE-LIKE PROTEIN | Glycosylase |
| 23094 | 2899 | DIHYDROFLAVONOL 4-REDUCTASE | Reductase |
| 23097 | 2900 | N-HYDROXYCINNAMOYL/BENZOYLTRANSFERASE-LIKE PROTEIN | Transferases |
| 23116 | 2901 | RECEPTOR KINASE-LIKE PROTEIN | Kinase, Protein |
| 23148 | 2902 | INORGANIC PHOSPHATE TRANSPORTER (DBJ BAA34390.1) | Transporter |
| 23149 | 2903 | PHOSPHATE TRANSPORTER (GB AAB17265.1) | Transporter |
| 23150 | 2904 | INORGANIC PHOSPHATE TRANSPORTER (DBJ BAA24281.1) | Transporter |
| 23151 | 2905 | INORGANIC PHOSPHATE TRANSPORTER (DBJ BAA24282.1) | Transporter |
| 23157 | 2906 | 1-AMINOCYCLOPROPANE-1-CARBOXYLATE OXIDASE | Oxidase |
| 23158 | 2907 | 1-AMINOCYCLOPROPANE-1-CARBOXYLATE OXIDASE | Oxidase |
| 23173 | 2908 | N-CARBAMYL-L-AMINO ACID AMIDOHYDROLASE-LIKE PROTEIN | Hydrolase |
| 23174 | 2909 | SUCROSE TRANSPORTER PROTEIN | Transporter |
| 23189 | 2910 | BETA-KETOACYL-COA SYNTHASE | Synthase |
| 23202 | 2911 | DIMETHYLANILINE MONOOXYGENASE-LIKE | Oxygenases |
| 23216 | 2912 | CELLULOSE SYNTHASE CATALYTIC SUBUNIT-LIKE PROTEIN | Synthase |
| 23265 | 2913 | RIBOSE 5-PHOSPHATE ISOMERASE[PUTATIVE] | Isomerase |
| 23276 | 2914 | TERPENE CYCLASE/SYNTHASE | Cyclase |
| 23281 | 2915 | DNA-3-METHYLADENINE GLYCOSYLASE I[PUTATIVE] | Glycosylase |
| 23283 | 2916 | RECEPTOR-LIKE PROTEIN KINASE | Kinase, Protein |
| 23296 | 2917 | POLYGALACTURONASE-LIKE PROTEIN | Glycosylase |
| 23297 | 2918 | POLYGALACTURONASE | Glycosylase |
| 23331 | 2919 | DIMETHYLANILINE MONOOXYGENASE (N-OXIDE-FORMING)-LIKE PROTEIN | Oxygenases |
| 23341 | 2920 | PECTINACETYLESTERASE | Esterase |
| 23343 | 2921 | BETA-AMYLASE-LIKE | Glycosylase |

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| 23351 | 2922 | UREA ACTIVE TRANSPORTER-LIKE PROTEIN | Transporter |
| 23377 | 2923 | SUBTILISIN-LIKE PROTEASE | Protease |
| 23378 | 2924 | SUBTILISIN-LIKE PROTEASE | Protease |
| 23379 | 2925 | LIPASE/HYDROLASE GDSL-like -motif | Lipase |
| 23380 | 2926 | PEPTIDYL-PROLYL CIS-TRANS ISOMERASE FKBP-TYPE [PUTATIVE] | Isomerase |
| 23384 | 2927 | DNA POLYMERASE III, GAMMA SUBUNIT[PUTATIVE] | Polymerase |
| 23390 | 2928 | RECEPTOR-LIKE PROTEIN KINASE | Kinase, Protein |
| 23391 | 2929 | TYROSINE-SPECIFIC PROTEIN PHOSPHATASE-LIKE PROTEIN | Phosphatase |
| 23392 | 2930 | RECEPTOR KINASE-LIKE PROTEIN | Kinase, Protein |
| 23396 | 2931 | RECEPTOR PROTEIN KINASE-LIKE PROTEIN | Kinase, Protein |
| 23403 | 2932 | LIPASE/HYDROLASE GDSL-like -motif | Lipase |
| 23405 | 2933 | MAGNESIUM CHELATASE SUBUNIT OF PROTOCHLOROPHYLLIDE REDUCTASE | Chelatase |
| 23407 | 2934 | LIPASE/HYDROLASE GDSL-like -motif | Lipase |
| 23408 | 2935 | LIPASE/HYDROLASE GDSL-like -motif | Lipase |
| 23420 | 2936 | SERINE/THREONINE PROTEIN KINASE-LIKE PROTEIN | Kinase, Protein |
| 23449 | 2937 | POTASSIUM CHANNEL OUTWARD RECTIFYING KCO | Channel |
| 23467 | 2938 | KINASE[PUTATIVE] | Kinase, Protein |
| 23469 | 2939 | PROTEIN KINASE-LIKE PROTEIN | Kinase, Protein |
| 23511 | 2940 | PEROXIDASE | Oxidase |
| 23516 | 2941 | S-RIBONUCLEASE BINDING PROTEIN[PUTATIVE] | Nuclease |
| 23518 | 2942 | SERINE/THREONINE KINASE-LIKE | Kinase, Protein |
| 23556 | 2943 | MEMBRANE CHANNEL PROTEIN-LIKE; AQUAPORIN (TONOPLAST INTRINSIC PROTEIN)-LIKE | Channel |
| 23561 | 2944 | PECTIN METHYLESTERASE-LIKE | Esterase |
| 23592 | 2945 | PYROPHOSPHATE-FRUCTOSE-6-PHOSPHATE PHOSPHOTRANSFERASE-LIKE PROTEIN | 1- Transferases |
| 23595 | 2946 | ADENYLATE KINASE[PUTATIVE] | Kinase |
| 23617 | 2947 | PHOSPHORIBOSYLANTHRANILATE TRANSFERASE- LIKE PROTEIN | Transferases |
| 23618 | 2948 | XYLOGLUCAN ENDO-1,4-BETA-D-GLUCANASE | Glycosylase |

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| 23621 | 2949 | LACCASE (DIPHENOL OXIDASE) | Oxidase |
| 23622 | 2950 | TERPENE SYNTHASE | Synthase |
| 23625 | 2951 | POLYGALACTURONASE | Glycosylase |
| 23633 | 2952 | INDOLE-3-GLYCEROL PHOSPHATE SYNTHASE | Synthase |
| 23649 | 2953 | RECEPTOR-LIKE PROTEIN KINASE | Kinase, Protein |
| 23651 | 2954 | LIGAND-GATED ION CHANNEL PROTEIN-LIKE; GLUTAMATE RECEPTOR-LIKE | Channel |
| 23652 | 2955 | LIGAND-GATED ION CHANNEL PROTEIN-LIKE; GLUTAMATE RECEPTOR-LIKE | Channel |
| 23656 | 2956 | PECTINESTERASE-LIKE; ALSO HIGHLY SIMILAR TO L- ASCORBATE OXIDASE AND POLLEN-SPECIFIC PROTEIN[PUTATIVE] | Oxidase |
| 23685 | 2957 | RECEPTOR PROTEIN KINASE-LIKE PROTEIN | Kinase, Protein |
| 23695 | 2958 | PANTOATE-BETA-ALANINE LIGASE | Ligase |
| 23701 | 2959 | PECTATE LYASE | Lyase |
| 23704 | 2960 | ANTHRANILATE N-BENZOYLTRANSFERASE | Transferases |
| 23718 | 2961 | FATTY ACID ELONGASE; BETA-KETOACYL-COA SYNTHASE-LIKE PROTEIN | Synthase |
| 23729 | 2962 | PECTIN METHYLESTERASE | Esterase |
| 23730 | 2963 | SUCROSE SYNTHASE | Synthase |
| 23738 | 2964 | PHYTOCHELATIN SYNTHETASE[PUTATIVE], PROTEIN CONTAINS SIMILARITY TO | Synthase |
| 23747 | 2965 | XYLOSIDASE | Glycosylase |
| 23774 | 2966 | AMINO ACID PERMEASE 6 (EMB CAA65051.1) | Transporter |
| 23777 | 2967 | RECEPTOR PROTEIN KINASE | Kinase, Protein |
| 23780 | 2968 | ANTHOCYANIDIN-3-GLUCOSIDE RHAMNOSYLTRANSFERASE-LIKE | Transferases |
| 23784 | 2969 | FRO2-LIKE PROTEIN; NADPH OXIDASE-LIKE | Oxidase |
| 23785 | 2970 | FRO1-LIKE PROTEIN; NADPH OXIDASE-LIKE | Oxidase |
| 23786 | 2971 | ELICITOR-INDUCIBLE RECEPTOR-LIKE PROTEIN EIR[PUTATIVE] | Receptor |
| 23787 | 2972 | RECEPTOR PROTEIN KINASE-LIKE | Kinase, Protein |
| 23788 | 2973 | RECEPTOR PROTEIN KINASE-LIKE | Kinase, Protein |

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| 23789 | 2974 | RECEPTOR PROTEIN KINASE-LIKE | Kinase, Protein |
| 23792 | 2975 | METHIONINE S-METHYLTRANSFERASE (GB AAD49574.1) | Transferases |
| 23844 | 2976 | ABC TRANSPORTER[PUTATIVE] | Transporter |
| 23870 | 2977 | 11-BETA-HYDROXYSTEROID DEHYDROGENASE-LIKE | Dehydrogenases |
| 23871 | 2978 | 11-BETA-HYDROXYSTEROID DEHYDROGENASE-LIKE | Dehydrogenases |
| 23876 | 2979 | PROTEIN TRANSPORT PROTEIN SEC12P-LIKE | Transporter |
| 23880 | 2980 | 11-BETA-HYDROXYSTEROID DEHYDROGENASE-LIKE | Dehydrogenases |
| 23881 | 2981 | 11-BETA-HYDROXYSTEROID DEHYDROGENASE-LIKE | Dehydrogenases |
| 23886 | 2982 | UDP-GLUCOSE:PROTEIN TRANSGLYCOSYLASE; REVERSIBLY GLYCOSYLATED POLYPEPTIDE | Glycosylase |
| 23888 | 2983 | OXIDOREDUCTASE[PUTATIVE] | Reductase |
| 23937 | 2984 | ACID PHOSPHATASE | Phosphatase |
| 23942 | 2985 | GIBBERELLIN 20-OXIDASE-LIKE PROTEIN | Oxidase |
| 23946 | 2986 | RECEPTOR PROTEIN KINASE-LIKE | Kinase, Protein |
| 23953 | 2987 | WAX SYNTHASE[PUTATIVE], PROTEIN CONTAINS SIMILARITY TO | Synthase |
| 23956 | 2988 | AUTOCRINE MOTILITY FACTOR RECEPTOR[PUTATIVE] | Receptor |
| 23957 | 2989 | TREHALOSE-6-PHOSPHATE PHOSPHATASE | Phosphatase |
| 23959 | 2990 | PECTINESTERASE-LIKE; STRONG SIMILARITY TO POLLEN-SPECIFIC PROTEIN[PUTATIVE] | Esterase |
| 23960 | 2991 | PECTINESTERASE | Esterase |
| 23961 | 2992 | PECTINESTERASE | Esterase |
| 23967 | 2993 | RECEPTOR-LIKE PROTEIN KINASE | Kinase, Protein |
| 23982 | 2994 | POTASSIUM/PROTON ANTIporter-LIKE PROTEIN | Transporter |
| 23985 | 2995 | PEPTIDASE[PUTATIVE] | Protease |
| 23986 | 2996 | SERINE PROTEASE-LIKE PROTEIN | Protease |
| 23987 | 2997 | PROTEIN PHOSPHATASE-2C; PP2C-LIKE PROTEIN | Phosphatase |
| 23988 | 2998 | PROTEIN KINASE[PUTATIVE] | Kinase, Protein |
| 23992 | 2999 | GIBBERELLIN 20-OXIDASE (EMB CAA58294.1) | Oxidase |

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| 23994 | 3000 | FRUCTOKINASE 1 | Kinase |
| 24000 | 3001 | PEROXIDASE | Oxidase |
| 24004 | 3002 | MANDELONITRILE LYASE-LIKE PROTEIN | Lyase |
| 24009 | 3003 | MYOSIN HEAVY CHAIN KINASE[PUTATIVE], CONTAINS SIMILARITY TO | Kinase, Protein |
| 24021 | 3004 | DIHYDRODIPICOLINATE REDUCTASE-LIKE PROTEIN | Reductase |
| 24039 | 3005 | HYALURONAN MEDIATED MOTILITY RECEPTOR-LIKE PROTEIN | Receptor |
| 24068 | 3006 | BETA-CAROTENE HYDROXYLASE | Hydroxylase |
| 24091 | 3007 | ORNITHINE CYCLODEAMINASE[PUTATIVE PROTEIN] CONTAINS SIMILARITY TO] | Deaminase |
| 24119 | 3008 | PROTOCHLOROPHYLLIDE REDUCTASE; OXIDOREDUCTASE REQUIRED FOR SHOOT APEX DEVELOPMENT | Reductase |
| 24120 | 3009 | PROTOCHLOROPHYLLIDE REDUCTASE; OXIDOREDUCTASE REQUIRED FOR SHOOT APEX DEVELOPMENT | Reductase |
| 24123 | 3010 | CYCLIC NUCLEOTIDE-REGULATED ION CHANNEL (EMB CAA76178.1) | Channel |
| 24142 | 3011 | RECEPTOR PROTEIN KINASE-LIKE PROTEIN | Kinase, Protein |
| 24147 | 3012 | PECTINESTERASE | Esterase |
| 24168 | 3013 | ALDO/KETO REDUCTASE-LIKE PROTEIN | Reductase |
| 24191 | 3014 | CAFFEIC ACID 3-O-METHYLTRANSFERASE-LIKE PROTEIN | Transferases |
| 24199 | 3015 | RECEPTOR PROTEIN KINASE-LIKE PROTEIN | Kinase, Protein |
| 24202 | 3016 | METHYLTRANSFERASE-LIKE PROTEIN , RIBOSOMAL PROTEIN L11 | Transferases |
| 24209 | 3017 | FLAVONOL 3-O-GLUCOSYLTRANSFERASE-LIKE PROTEIN | Transferases |
| 24210 | 3018 | ETHYLENE-FORMING-ENZYME-LIKE DIOXYGENASE | Oxygenases |
| 24211 | 3019 | FLAVONOL 3-O-GLUCOSYLTRANSFERASE-LIKE PROTEIN | Transferases |
| 24216 | 3020 | FLAVONOL 3-O-GLUCOSYLTRANSFERASE-LIKE | Transferases |
| 24224 | 3021 | IAA-AMINO ACID HYDROLASE HOMOLOG ILL3 (GB AAC31939.1) | Hydrolase |

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| 24226 | 3022 | O-METHYLTRANSFERASE | Transferases |
| 24229 | 3023 | PROTOCHLOROPHYLLIDE OXIDOREDUCTASE A NADPH (GB AAC49043.1) | Reductase |
| 24235 | 3024 | CYCLIC NUCLEOTIDE AND CALMODULIN-REGULATED ION CHANNEL | Channel |
| 24248 | 3025 | RECEPTOR-PROTEIN KINASE-LIKE PROTEIN | Kinase, Protein |
| 24260 | 3026 | 1,4-BENZOQUINONE REDUCTASE-LIKE; TRP REPRESSOR BINDING PROTEIN-LIKE | Reductase |
| 24269 | 3027 | SERINE/THREONINE-SPECIFIC PROTEIN KINASE-LIKE PROTEIN | Kinase, Protein |
| 24291 | 3028 | TRYPTOPHAN SYNTHASE BETA CHAIN 1 PRECURSOR (SP P14671) | Synthase |
| 24306 | 3029 | PYRUVATE DECARBOXYLASE (GB AAB16855.1) | Decarboxylase |
| 24315 | 3030 | LIPASE/HYDROLASE GDSL-like -motif | Lipase |
| 24328 | 3031 | BETA-1,3-GLUCANASE-LIKE PROTEIN | Glycosylase |
| 24335 | 3032 | S-ADENOSYL-L-METHIONINE:SALICYLIC ACID CARBOXYL METHYLTRANSFERASE-LIKE PROTEIN | Transferases |
| 24342 | 3033 | WAX SYNTHASE-LIKE PROTEIN | Synthase |
| 24343 | 3034 | WAX SYNTHASE-LIKE PROTEIN | Synthase |
| 24344 | 3035 | WAX SYNTHASE[PUTATIVE], PROTEIN CONTAINS SIMILARITY TO | Synthase |
| 24345 | 3036 | WAX SYNTHASE-LIKE PROTEIN | Synthase |
| 24346 | 3037 | WAX SYNTHASE-LIKE PROTEIN | Synthase |
| 24347 | 3038 | WAX SYNTHASE-LIKE PROTEIN | Synthase |
| 24348 | 3039 | WAX SYNTHASE-LIKE PROTEIN | Synthase |
| 24369 | 3040 | PECTIN METHYLESTERASE [PUTATIVE] | Esterase |
| 24373 | 3041 | POTASSIUM CHANNEL OUTWARD RECTIFYING KCO | Channel |
| 24380 | 3042 | BETA-AMYLASE | Glycosylase |
| 24382 | 3043 | PECTATE LYASE | Lyase |
| 24393 | 3044 | SERINE/THREONINE-SPECIFIC KINASE LIKE PROTEIN | Kinase, Protein |
| 24414 | 3045 | RECEPTOR PROTEIN KINASE-LIKE PROTEIN | Kinase, Protein |
| 24418 | 3046 | NICOTIANAMINE SYNTHASE | Synthase |

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| 24436 | 3047 | S-ADENOSYLMETHIONINE:2-DEMETHYLMENAQUINONE METHYLTRANSFERASE-LIKE | Transferases |
| 24440 | 3048 | S-ADENOSYL-L-METHIONINE:SALICYLIC ACID CARBOXYL METHYLTRANSFERASE-LIKE PROTEIN | Transferases |
| 24443 | 3049 | CARBONIC ANHYDRASE[PUTATIVE, PROTEIN CONTAINS SIMILARITY TO] | Anhydrase |
| 24469 | 3050 | BETA-1,3-GLUCANASE-LIKE PROTEIN | Glycosylase |
| 24473 | 3051 | PHOSPHOFRUCTO-1-KINASE, PYROPHOSPHATE-DEPENDENT PHOSPHOFRUCTO-1-KINASE-LIKE PROTEIN | Kinase |
| 24475 | 3052 | IAA-AMINO ACID HYDROLASE HOMOLOG 1 PRECURSOR (SP P54969) | Hydrolase |
| 24476 | 3053 | IAA-AMINO ACID HYDROLASE (GB AAC04866.1) | Hydrolase |
| 24483 | 3054 | ZINC PROTEASE PQQL-LIKE PROTEIN | Protease |
| 24484 | 3055 | HISTONE ACETYLTRANSFERASE HAT B | Transferases |
| 24486 | 3056 | SERINE O-ACETYLTRANSFERASE (EC 2.3.1.30) SAT-52 (PIR S71207) | Transferases |
| 24489 | 3057 | PROTEIN KINASE[PUTATIVE] | Kinase, Protein |
| 24506 | 3058 | CYTOKININ OXIDASE | Oxidase |
| 24512 | 3059 | LYCOPENE EPSILON CYCLASE | Cyclase |
| 24518 | 3060 | AUXIN TRANSPORT PROTEIN EIR1 (GB AAC39513.1) | Transporter |
| 24528 | 3061 | PHOSPHATIDYLSERINE DECARBOXYLASE | Decarboxylase |
| 24555 | 3062 | AAA-TYPE ATPASE[PUTATIVE] | ATPase |
| 24560 | 3063 | XYLOGLUCAN ENDOTRANSGLYCOSYLASE | Glycosylase |
| 24561 | 3064 | XYLOGLUCAN ENDOTRANSGLYCOSYLASE | Glycosylase |
| 24562 | 3065 | ENDOXYLOGLUCAN TRANSFERASE (GB AAD45127.1) | Transferases |
| 24566 | 3066 | ADENOSYLMETHIONINE-8-AMINO-7-OXONONANOATE AMINOTRANSFERASE-LIKE PROTEIN | Transferases |
| 24591 | 3067 | N-HYDROXYCINNAMOYL/BENZOYLTRANSFERASE | Transferases |
| 24592 | 3068 | BRANCHED-CHAIN AMINO ACID AMINOTRANSFERASE-LIKE PROTEIN | Transferases |
| 24596 | 3069 | ANTHRANILATE SYNTHASE BETA CHAIN | Synthase |

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| 24601 | 3070 | CYCLIC NUCLEOTIDE AND CALMODULIN-REGULATED ION CHANNEL (EMB CAB40130.1) | Channel |
| 24604 | 3071 | DNA-3-METHYLADENINE GLYCOSYLASE[PUTATIVE] | Glycosylase |
| 24616 | 3072 | BETA-1,3 GLUCANASE - LIKE PROTEIN BETA-1,3 GLUCANASE, POPULUS ALBA X POPULUS TREMULA, EMBL:AF230109 | Glycosylase |
| 24622 | 3073 | RECEPTOR-LIKE PROTEIN KINASE | Kinase, Protein |
| 24627 | 3074 | PHOSPHOESTERASE [CONTAINS SIMILARITY TO] | Esterase |
| 24637 | 3075 | RECEPTOR-LIKE PROTEIN KINASE | Kinase, Protein |
| 24638 | 3076 | ALPHA-HYDROXYNITRILE LYASE, POLYNEURIDINE ALDEHYDE ESTERASE-LIKE; ALSO SIMILAR TO ALPHA-HYDROXYNITRILE LYASE | Lyase |
| 24646 | 3077 | PEROXIDASE | Oxidase |
| 24647 | 3078 | PEROXIDASE | Oxidase |
| 24655 | 3079 | BETA 1-3 GLUCANASE - LIKE PROTEIN BETA 1-3 GLUCANASE, VITIS VINIFERA, EMBL:VVI277900 | Glycosylase |
| 24656 | 3080 | CINNAMOYL-COA REDUCTASE - LIKE PROTEIN CINNAMOYL-COA REDUCTASE, CIDER TREE, PIR:T10733 | Reductase |
| 24659 | 3081 | PROTEIN KINASE - LIKE PROTEIN KINASE ATN1, ARABIDOPSIS THALIANA, PIR:S61766 | Kinase, Protein |
| 24661 | 3082 | SERINE/THREONINE-SPECIFIC PROTEIN KINASE NPK15, NICOTIANA TABACUM, PIR:S52578[PUTATIVE] | Kinase, Protein |
| 24680 | 3083 | CARBOHYDRATE KINASE, PFKB, ARCHAEoglobus FULGIDUS, PIR:A69300[PUTATIVE] | Kinase |
| 24701 | 3084 | RECEPTOR-LIKE PROTEIN KINASE PRECURSOR - LIKE RECEPTOR-LIKE PROTEIN KINASE PRECURSOR, MADAGASCAR PERIWINKLE, PIR:T10060 | Kinase, Protein |
| 24708 | 3085 | PROTEIN KINASE - LIKE SERINE/THREONINE/TYROSINE-SPECIFIC PROTEIN KINASE APK1, ARABIDOPSIS THALIANA, PIR:S28615 | Kinase, Protein |
| 24710 | 3086 | COPPER TRANSPORT PROTEIN | Transporter |
| 24711 | 3087 | COPPER TRANSPORT PROTEIN - LIKE | Transporter |
| 24714 | 3088 | HEXOSYLTRANSFERASE - LIKE PROTEIN | Transferases |

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| 24733 | 3089 | RECEPTOR-LIKE PROTEIN KINASE RECEPTOR-LIKE PROTEIN KINASE, ARABIDOPSIS THALIANA, PIR:T47481 | Kinase, Protein |
| 24734 | 3090 | RECEPTOR-LIKE PROTEIN KINASE RECEPTOR-LIKE PROTEIN KINASE, ARABIDOPSIS THALIANA, PIR:T47481 | Kinase, Protein |
| 24759 | 3091 | ZINC TRANSPORTER ZIP2 - LIKE Z25114[PUTATIVE] | Transporter |
| 24760 | 3092 | 1-AMINOCYCLOPROPANE-1-CARBOXYLATE OXIDASE - LIKE PROTEIN 1-AMINOCYCLOPROPANE-1-CARBOXYLATE OXIDASE KIDNEY BEAN, PIR:T10818 | Oxidase |
| 24761 | 3093 | 1-AMINOCYCLOPROPANE-1-CARBOXYLATE OXIDASE - LIKE PROTEIN 1-AMINOCYCLOPROPANE-1-CARBOXYLATE OXIDASE KIDNEY BEAN, PIR:T10818 | Oxidase |
| 24765 | 3094 | GLUCURONOSYL TRANSFERASE - LIKE PROTEIN GLUCURONOSYL TRANSFERASE HOMOLOG, RIPENING-RELATED, LYCOPERSICON ESCULENTUM, PIR:S39507 | Transferases |
| 24766 | 3095 | GLUCURONOSYL TRANSFERASE - LIKE PROTEIN GLUCURONOSYL TRANSFERASE HOMOLOG, RIPENING-RELATED, LYCOPERSICON ESCULENTUM, PIR:S39507 | Transferases |
| 24771 | 3096 | SERINE/THREONINE-SPECIFIC PROTEIN KINASE - LIKE PUTATIVE PROTEIN SERINE /THREONINE KINASE, SORGHUM BICOLOR, EMBL:SBRLK1 | Kinase, Protein |
| 24772 | 3097 | SERINE/THREONINE-SPECIFIC PROTEIN KINASE - LIKE PUTATIVE PROTEIN SERINE /THREONINE KINASE, SORGHUM BICOLOR, EMBL:SBRLK1 | Kinase, Protein |
| 24773 | 3098 | SERINE/THREONINE-SPECIFIC PROTEIN KINASE - LIKE PUTATIVE PROTEIN SERINE /THREONINE KINASE, SORGHUM BICOLOR, EMBL:SBRLK1 | Kinase, Protein |
| 24774 | 3099 | SERINE/THREONINE-SPECIFIC PROTEIN KINASE - LIKE PUTATIVE PROTEIN SERINE /THREONINE KINASE, SORGHUM BICOLOR, EMBL:SBRLK1 | Kinase, Protein |
| 24777 | 3100 | RECEPTOR-LIKE PROTEIN KINASE PRECURSOR - LIKE RECEPTOR-LIKE PROTEIN KINASE PRECURSOR, MADAGASCAR PERIWINKLE, PIR:T10060 | Kinase, Protein |

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| 24781 | 3101 | SERINE /THREONINE KINASE - LIKE PUTATIVE SERINE /THREONINE KINASE, SORGHUM BICOLOR, EMBL:SBRLK1 | Kinase, Protein |
| 24782 | 3102 | GTP CYCLOHYDROLASE II / 3,4-DIHYDROXY-2-BUTANONE-4-PHOSPHATE SYNTHASE - LIKE PROTEIN GTP CYCLOHYDROLASE II / 3,4-DIHYDROXY-2-BUTANONE-4-PHOSPHATE SYNTHASE, ARABIDOPSIS THALIANA, EMBL:ATAJ0053 | Synthase |
| 24784 | 3103 | TYROSINE PHOSPHATASE-LIKE PROTEIN, PTPLB, MUSCULUS, EMBL:AF169286[PUTATIVE] | Phosphatase |
| 24788 | 3104 | SUBTILISIN-LIKE PROTEASE - LIKE PROTEIN SUBTILISIN-LIKE PROTEASE AIR3, ARABIDOPSIS THALIANA, EMBL:AF098632 | Protease |
| 24815 | 3105 | PROTEIN KINASE - LIKE PROTEIN KINASE 1, POPULUS NIGRA, EMBL:AB041503 | Kinase, Protein |
| 24816 | 3106 | PROTEIN KINASE - LIKE PROTEIN KINASE 1, POPULUS NIGRA, EMBL:AB041503 | Kinase, Protein |
| 24830 | 3107 | TRNA INTRON ENDONUCLEASE - LIKE PROTEIN TRNA INTRON ENDONUCLEASE, ARABIDOPSIS THALIANA, EMBL:AB036339 | Nuclease |
| 24834 | 3108 | RECEPTOR LIKE PROTEIN KINASE RECEPTOR LIKE PROTEIN KINASE, ARABIDOPSIS THALIANA, PIR:T47484 | Kinase, Protein |
| 24835 | 3109 | RECEPTOR LIKE PROTEIN KINASE RECEPTOR LIKE PROTEIN KINASE, ARABIDOPSIS THALIANA, PIR:T47484 | Kinase, Protein |
| 24837 | 3110 | RECEPTOR LIKE PROTEIN KINASE RECEPTOR LIKE PROTEIN KINASE, ARABIDOPSIS THALIANA, EMBL:AL138657 | Kinase, Protein |
| 24838 | 3111 | RECEPTOR LIKE PROTEIN KINASE RECEPTOR LIKE PROTEIN KINASE, ARABIDOPSIS THALIANA, EMBL:AL138657 | Kinase, Protein |
| 24839 | 3112 | RECEPTOR-LIKE PROTEIN KINASE RECEPTOR-LIKE PROTEIN KINASE, ARABIDOPSIS THALIANA, PIR:T47473 | Kinase, Protein |

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| 24861 | 3113 | IMIDAZOLEGLYCEROL-PHOSPHATE SYNTHASE SUBUNIT H - LIKE IMIDAZOLEGLYCEROL-PHOSPHATE SYNTHASE SUBUNIT H HOMOLOG, ARCHAEoglobus FULGIDUS, PIR:E69313 | Synthase |
| 24884 | 3114 | HIGH-AFFINITY NITRATE TRANSPORTER ACH1 - LIKE PROTEIN HIGH-AFFINITY NITRATE TRANSPORTER ACH1, ARABIDOPSIS THALIANA, EMBL:AF019748 | Transporter |
| 24885 | 3115 | HIGH AFFINITY NITRATE TRANSPORTER PROTEIN - LIKE PROBABLE HIGH AFFINITY NITRATE TRANSPORTER PROTEIN, GLYCINE MAX, PIR:T06237 | Transporter |
| 24897 | 3116 | S-RECEPTOR KINASE HOMOLOG 2 PRECURSOR S- RECEPTOR KINASE HOMOLOG 2 PRECURSOR, ARABIDOPSIS THALIANA, PIR:S27754 | Kinase, Protein |
| 24899 | 3117 | PHYTOCHELATIN SYNTHETASE - LIKE PROTEIN PUTATIVE PHYTOCHELATIN SYNTHETASE, ARABIDOPSIS THALIANA, EMBL:ATH6787 | Synthase |
| 24902 | 3118 | PHYTOCHELATIN SYNTHETASE - LIKE PUTATIVE PHYTOCHELATIN SYNTHETASE, ARABIDOPSIS THALIANA, EMBL:ATH6787[PUTATIVE] | Synthase |
| 24923 | 3119 | ANTHOCYANIN 5-AROMATIC ACYLTRANSFERASE - LIKE PROTEIN ANTHOCYANIN 5-AROMATIC ACYLTRANSFERASE, GENTIANA TRIFLORA, EMBL:AB010708 | Transferases |
| 24942 | 3120 | RECEPTOR-LIKE PROTEIN KINASE PRECURSOR - LIKE RECEPTOR-LIKE PROTEIN KINASE PRECURSOR, MADAGASCAR PERIWINKLE, PIR:T10060 | Kinase, Protein |
| 24955 | 3121 | LEUCINE-RICH RECEPTOR-LIKE PROTEIN KINASE - LIKE PROTEIN LEUCINE-RICH RECEPTOR-LIKE PROTEIN KINASE LRPKM1, MALUS DOMESTICA, EMBL:AF053127 | Kinase, Protein |
| 24964 | 3122 | PROTEIN KINASE-LIKE TRANSMEMBRANE PROTEIN TMKLI PRECURSOR, ARABIDOPSIS THALIANA, EMBL:ATTMKLI[PUTATIVE] | Kinase, Protein |

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| 24965 | 3123 | PHOSPHOFRUCTO-1-KINASE, PYROPHOSPHATE-DEPENDENT PHOSPHOFRUCTO-1-KINASE - LIKE PROTEIN . PYROPHOSPHATE-DEPENDENT PHOSPHOFRUCTO-1-KINASE, PRUNUS ARMENIACA, EMBL:U93272 | Kinase |
| 24975 | 3124 | PECTIN METHYL-ESTERASE - LIKE PROTEIN PECTIN METHYL ESTERASE PEST2, SOLANUM TUBEROSUM, EMBL:AF152172 | Esterase |
| 25021 | 3125 | IRON-REGULATED TRANSPORTER - LIKE PROTEIN IRON-REGULATED TRANSPORTER 1, LYCOPERSICON ESCULENTUM, EMBL:AF136579 | Transporter |
| 25028 | 3126 | RECEPTOR-LIKE PROTEIN KINASE 5, ARABIDOPSIS THALIANA, PIR:S27756[PUTATIVE] | Kinase, Protein |
| 25053 | 3127 | GLUTATHIONE S-TRANSFERASE-LIKE PROTEIN | Transferases |
| 25058 | 3128 | DEHYDROGENASE | Dehydrogenases |
| 25065 | 3129 | TRANSPORTIN-SR[PUTATIVE] | Transporter |
| 25073 | 3130 | PEPTIDE TRANSPORTER | Transporter |
| 25076 | 3131 | RECEPTOR - LIKE PROTEIN KINASE - LIKE PROTEIN SERINE/THREONINE KINASE RLK1, SORGHUM BICOLOR, EMBL:SBRLK1 | Kinase, Protein |
| 25078 | 3132 | NITRATE TRANSPORTER NTL1 - LIKE PROTEIN NITRATE TRANSPORTER NTL1, ARABIDOPSIS THALIANA, EMBL:AF073361 | Transporter |
| 25084 | 3133 | 1-DEOXY-D-XYLULOSE 5-PHOSPHATE REDUCTOISOMERASE (DXR) | Isomerase |
| 25102 | 3134 | DIHYDRONEOPTERIN ALDOLASE-LIKE PROTEIN | Aldolase |
| 25121 | 3135 | LIPASE/HYDROLASE-LIKE PROTEIN | Lipase |
| 25122 | 3136 | PECTATE LYASE | Lyase |
| 25127 | 3137 | BETA-1,3-GLUCANASE-LIKE PROTEIN[PUTATIVE] | Glycosylase |
| 25137 | 3138 | KINASE[PUTATIVE] | Kinase, Protein |
| 25145 | 3139 | RECEPTOR-LIKE PROTEIN KINASE[PUTATIVE] | Kinase, Protein |
| 25155 | 3140 | ACETYLTRANSFERASE[PUTATIVE] | Transferases |
| 25160 | 3141 | ACYLTRANSFERASE-LIKE PROTEIN | Transferases |

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| 25161 | 3142 | GLUTAMATE-1-SEMIALDEHYDE 2,1-AMINOMUTASE 1 PRECURSOR (GSA 1) (GLUTAMATE-1-SEMIALDEHYDE AMINOTRANSFERASE 1) (GSA-AT 1) (SP P42799) | Transferases |
| 25162 | 3143 | FLAVONOL SYNTHASE | Synthase |
| 25163 | 3144 | FLAVONOL SYNTHASE | Synthase |
| 25164 | 3145 | 1-AMINOCYCLOPROPANE-1-CARBOXYLIC ACID OXIDASE-LIKE PROTEIN | Oxidase |
| 25175 | 3146 | RECEPTOR-LIKE PROTEIN KINASE | Kinase, Protein |
| 25185 | 3147 | BETA-GALACTOSIDASE (EMB CAB64746.1) | Glycosylase |
| 25189 | 3148 | AMINO ACID TRANSPORTER AAP4 (PIR S51169) | Transporter |
| 25193 | 3149 | HISTIDINOL DEHYDROGENASE | Dehydrogenases |
| 25197 | 3150 | RECEPTOR-LIKE PROTEIN KINASE | Kinase, Protein |
| 25198 | 3151 | PROTEIN KINASE[PUTATIVE] | Kinase, Protein |
| 25214 | 3152 | PEROXIDASE ATP3A (EMB CAA67340.1) | Oxidase |
| 25215 | 3153 | PEROXIDASE ATP3A HOMOLOG | Oxidase |
| 25216 | 3154 | PEROXIDASE (EMB CAA67551.1) | Oxidase |
| 25225 | 3155 | ALTERNATIVE OXIDASE 2 (SP O22049) | Oxidase |
| 25229 | 3156 | 2-NITROPROPANE DIOXYGENASE-LIKE PROTEIN | Oxygenases |
| 25234 | 3157 | GTP CYCLOHYDROLASE II; 3,4-DIHYDROXY-2- BUTANONE-4-PHOSPHATE SYNTHASE (EMB CAA03884.1) | Synthase |
| 25261 | 3158 | BETA-XYLOSIDASE | Glycosylase |
| 25268 | 3159 | PECTIN METHYLESTERASE-LIKE PROTEIN | Esterase |
| 25278 | 3160 | CELLULOSE SYNTHASE CATALYTIC SUBUNIT | Synthase |
| 25283 | 3161 | BETA-1,3-GLUCANASE | Glycosylase |
| 25318 | 3162 | TREHALOSE-6-PHOSPHATE PHOSPHATASE | Phosphatase |
| 25326 | 3163 | RECEPTOR-LIKE PROTEIN KINASE | Kinase, Protein |
| 25352 | 3164 | RECEPTOR-LIKE KINASE[PUTATIVE] | Kinase, Protein |
| 25355 | 3165 | LECTIN-LIKE PROTEIN KINASE[PUTATIVE] | Kinase, Protein |
| 25357 | 3166 | ANTHOCYANIDIN-3-GLUCOSIDE RHAMNOSYLTRANSFERASE | Transferases |
| 25370 | 3167 | RECEPTOR PROTEIN KINASE-LIKE PROTEIN | Kinase, Protein |

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| 25371 | 3168 | RECEPTOR PROTEIN KINASE-LIKE PROTEIN | Kinase, Protein |
| 25373 | 3169 | XYLOGLUCAN ENDO-TRANSGLYCOSYLASE-LIKE PROTEIN | Glycosylase |
| 25383 | 3170 | RECEPTOR PROTEIN KINASE-LIKE PROTEIN[PUTATIVE] | Kinase, Protein |
| 25386 | 3171 | ARGININE METHYLTRANSFERASE[PUTATIVE] | Transferases |
| 25389 | 3172 | URIDYLYL TRANSFERASES-LIKE | Transferases |
| 25399 | 3173 | AMINO ACID TRANSPORTER PROTEIN-LIKE | Transporter |
| 25406 | 3174 | PROLYL 4-HYDROXYLASE, ALPHA SUBUNIT-LIKE PROTEIN | Hydroxylase |
| 25408 | 3175 | PROTEIN PHOSPHATASE 2C-LIKE PROTEIN | Phosphatase |
| 25412 | 3176 | 3-DEHYDROQUINATE SYNTHASE-LIKE PROTEIN | Synthase |
| 25415 | 3177 | ALPHA-MANNOSIDASE | Glycosylase |
| 25419 | 3178 | FERREDOXIN-NADP+ REDUCTASE | Reductase |
| 25422 | 3179 | CHALCONE ISOMERASE-LIKE PROTEIN | Isomerase |
| 25433 | 3180 | ELICITOR-INDUCIBLE RECEPTOR-LIKE PROTEIN[PUTATIVE] | Receptor |
| 25439 | 3181 | PEROXIDASE (EMB CAA66964.1) | Oxidase |
| 25443 | 3182 | S-ADENOSYL-L-METHIONINE:SALICYLIC ACID CARBOXYL METHYLTRANSFERASE-LIKE PROTEIN | Transferases |
| 25446 | 3183 | MANNAN ENDO-1,4-BETA-MANNOSIDASE | Glycosylase |
| 25469 | 3184 | UTP-GLUCOSE GLUCOSYLTRANSFERASE | Transferases |
| 25479 | 3185 | PROTEIN KINASE[PUTATIVE] | Kinase, Protein |
| 25492 | 3186 | PECTINESTERASE LIKE PROTEIN | Esterase |
| 25503 | 3187 | ZEAXANTHIN EPOXIDASE PRECURSOR | Oxidase |
| 25509 | 3188 | SUBTILISIN-TYPE PROTEASE-LIKE | Protease |
| 25510 | 3189 | DNA POLYMERASE ALPHA 1 | Polymerase |
| 25513 | 3190 | MAP3K-LIKE PROTEIN KINASE[PUTATIVE] | Kinase, Protein |
| 25515 | 3191 | ANTHRANILATE N- HYDROXYCINNAMOYL/BENZOYLTRANSFERASE-LIKE PROTEIN | Transferases |

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| 25516 | 3192 | ANTHRANILATE HYDROXYCINNAMOYL/BENZOYLTRANSFERASE-LIKE PROTEIN | N-Transferases |
| 25520 | 3193 | RECEPTOR PROTEIN KINASE-LIKE PROTEIN | Kinase, Protein |
| 25523 | 3194 | UDP-GLUCURONYLTRANSFERASE-LIKE PROTEIN | Transferases |
| 25528 | 3195 | RECEPTOR-LIKE PROTEIN KINASE | Kinase, Protein |
| 25536 | 3196 | CUCUMISIN-LIKE SERINE PROTEASE (GB AAC18851.1) | Protease |
| 25540 | 3197 | PEROXIDASE (EMB CAA66967.1) | Oxidase |
| 25543 | 3198 | N-ACETYLTRANSFERASE HOOKLESS1-LIKE PROTEIN | Transferases |
| 113old | 3199 | ACCELERATED CELL DEATH 2; RED CHLOROPHYLL CATABOLITE REDUCTASE [ARABIDOPSIS THALIANA] | Reductase |
| 12old | 3200 | LETHAL LEAF-SPOT 1 HOMOLOG LLS1 [DIOXYGENASE DOMAIN][ARABIDOPSIS THALIANA]. | Oxygenase |
| 13288old | 3201 | (EC 4.2.99.8) CYSC1 [SIMILARITY] - ARABIDOPSIS THALIANA. | |
| 15402old | 3202 | CYSTEINE SYNTHASE (EC 4.2.99.8) 3A, CYTOSOLIC - ARABIDOPSIS THALIANA. | Synthase |
| 15792old | 3203 | CYSTEINE SYNTHASE (EC 4.2.99.8) ISOFORM 5-8, CYTOSOLIC - ARABIDOPSIS THALIANA. | Synthase |
| 15851old | 3204 | CYSTEINE SYNTHASE (EC 4.2.99.8) ACS1 - ARABIDOPSIS THALIANA. | Synthase |
| 1678old | 3205 | CYSTEINE SYNTHASE; O-ACETYLSERINE(THIOL) LYASE [ARABIDOPSIS THALIANA]. | Synthase |
| 182old | 3206 | PROBABLE CYSTEINE SYNTHASE, CHLOROPLAST PRECURSOR (O-ACETYLSERINE SULFHYDRYLASE) (O- ACETYLSERINE (THIOL)-LYASE) (CSASE) (OAS-TL) (CS26). | Synthase |
| 18927old | 3207 | PUTATIVE CYSTEINE SYNTHASE; 39489-37437 [ARABIDOPSIS THALIANA]. | Synthase |
| 203old | 3208 | 5-METHYLTETRAHYDROPTEROYLTRIGLUTAMATE-- HOMOCYSTEINE METHYLTRANSFERASE (VITAMIN- B12-INDEPENDENT METHIONINE SYNTHASE ISOZYME) (COBALAMIN-INDEPENDENT METHIONINE SYNTHASE ISOZYME). | Transferases |

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| 21308old | 3209 | CYSTEINE SYNTHASE [ARABIDOPSIS THALIANA]. | Synthase |
| 21309old | 3210 | CYSTEINE SYNTHASE [ARABIDOPSIS THALIANA]. | Synthase |
| 23001old | 3211 | 4-DIPHOSPHOCYTIDYL-2C-METHYL-D-ERYTHRITOL SYNTHASE [ARABIDOPSIS THALIANA]. | Synthase |
| 23094old | 3212 | CYSTEINE SYNTHASE, CHLOROPLAST PRECURSOR (O- ACETYL SERINE SULFHYDRYLASE) (O-ACETYL SERINE (THIOL)-LYASE) (CSASE). | Synthase |
| 34209old | 3213 | CYSTEINE SYNTHASE [ARABIDOPSIS THALIANA]. | Synthase |
| 34659old | 3214 | CYSTEINE SYNTHASE ATCYSC1 [ARABIDOPSIS THALIANA]. | Synthase |
| 37280old | 3215 | CYSTEINE SYNTHASE, MITOCHONDRIAL PRECURSOR (O-ACETYL SERINE SULFHYDRYLASE) (O- ACETYL SERINE (THIOL)-LYASE) (CSASE). | Synthase |
| 37284old | 3216 | CYSTEINE SYNTHASE (O-ACETYL SERINE SULFHYDRYLASE) (O-ACETYL SERINE (THIOL)-LYASE) (CSASE). | Synthase |
| 39272old | 3217 | CHLOROPHYLL B SYNTHASE [ARABIDOPSIS THALIANA]. | Synthase |
| 40108old | 3218 | CYSTEINE SYNTHASE [ARABIDOPSIS THALIANA]. | Synthase |
| 40109old | 3219 | CYSTEINE SYNTHASE [ARABIDOPSIS THALIANA]. | Synthase |
| 42762old | 3220 | 5'-PHOSPHORIBOSYL-5-AMINOIMIDAZOLE SYNTHETASE. | Synthase |
| 42911old | 3221 | PUTATIVE CYSTEINE SYNTHASE [ARABIDOPSIS THALIANA]. | Synthase |
| 44492old | 3222 | SIMILAR TO NICOTIANA 5-EPI-ARISTOLOCHENE SYNTHASE (GB | Synthase |
| 44907old | 3223 | CYSTEINE SYNTHASE (EC 4.2.99.8) 3A - ARABIDOPSIS THALIANA. | Synthase |
| 44988old | 3224 | CYSTEINE SYNTHASE [ARABIDOPSIS THALIANA]. | Synthase |
| 45432old | 3225 | CYSTEINE SYNTHASE [ARABIDOPSIS THALIANA]. | Synthase |
| 46254old | 3226 | 3-DEOXY-D-ARABINO-HEPTULOSONATE PHOSPHATE SYNTHASE. | 7- Synthase |
| 7417old | 3227 | 2C-METHYL-D-ERYTHRITOL 2,4-CYCLODIPHOSPHATE SYNTHASE [ARABIDOPSIS THALIANA]. | Synthase |

Many annotations in publicly accessible data bases occur repeatedly, i.e. for various nucleic acid or amino acid sequences. The reasons for this are, to a minor extent, erroneous and/or redundant sequences and descriptions. To a major extent, this reflects the fact that proteins with the same function do indeed occur repeatedly in the genome. These different proteins can differ from each other for example by the regulation of their expression or by their cellular localization.

Many proteins belong to particular protein families. The skilled worker can draw conclusions with regard to the type of function, and thus also the possibility of an assay method for the polypeptide in question or its biological activity, from the protein family it belongs to. A description of such families of polypeptides and genes from Arabidopsis is obtainable for example in EP-A-1 033 405, but can also be found in the literature with which the skilled worker is familiar. Corresponding related information regarding the individual targets in Table 1 can be found in the document cited or in the general literature.

The analysis carried out for the purpose of the present invention, however, provides not only the general descriptions and the descriptions which are less suitable for the choice of herbicide targets in EP-A-1 033 405, but also the specificity of the polypeptide for the plant kingdom and the groups enzyme, receptor or channel (transporter) and more specific classes of these groups to which the proteins belong. The method according to the invention thus makes it possible to identify the particular suitability of a protein as target for finding lead structures for new herbicides exclusively with the aid of the method according to the invention. The classes which the polypeptides according to the invention were assigned to comprise, inter alia, acetylases, aldolases, amidases, amylases, anhydrases, arginases, ATPases, carboxylases, carrier-proteins, cellulases, channels, chelataes, chitinases, cyclases, deaminases, decarboxylases, dehydratases, dehydrogenases, desaturases, enolases, epimerases, esterases, furanases, furanosidases, galactosidases, galacturonases, glucanases, glucosidases, glucosylases, glucuronases, glycosylases, GTPases,

5 helicases, hydrolases, hydroxylases, isomerases, kinases, LACCases, lactonases, ligases, lipases, lyases, mannosidases, maturases, methylases, mutases, nucleases, nucleosidases, nucleotidases, oxidases, oxygenases, pectases, pectosidases, peptidases, permeases, phosphatases, phosphorylases, polymerases, proteases, racemases, receptors, reductases, sulfurylases, synthases, synthetases, transferases, transporters, transcriptases, xylanases and xylosidases.

10 The polypeptides which are identified by means of the method according to the invention are therefore particularly suitable as targets for finding new herbicidal active compounds. They are particularly suitable because they

- 15 a) have no homologous counterpart in animal organisms or in humans, according to the method according to the invention (determination of E-values, alignment of data bases),
- b) were selected with a view that they are enzymes with small ligands or else receptors or channels which can, as a rule, be modulated, i.e. inhibited or activated, by small organic molecules or peptides and are therefore in principle open to being influenced by an active compound, and
- 20 c) owing to the assignment to particular groups, make it possible for the skilled worker to select in a direct and obvious fashion assay methods which are suitable for the particular classes of polypeptides. To this end, the skilled worker can rely on the current literature or exploit the assay methods
- 25 described in the present application.

Subject-matter of the present invention is therefore furthermore the use of polypeptides found with the aid of the method according to the invention or of the nucleic acids encoding these polypeptides in methods for finding modulators of the polypeptides according to the invention or for finding new herbicidal compounds.

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Subject-matter of the present invention is in particular the use of one of the polypeptides of SEQ ID NO: 1 to SEQ ID NO: 3227 in methods for finding modulators of these polypeptides or for finding new herbicidal compounds.

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The subject-matter of the present invention is furthermore the use of polypeptides which exert at least the biological activity of one of the polypeptides according to the invention and which encompass an amino acid sequence which has at least 60% identity, preferably 80% identity, especially preferably 90% identity, very especially preferably 97% identity, with a sequence of SEQ ID NO: 1 to SEQ ID NO: 3227 over its entire length in methods for finding modulators of the polypeptides or for finding new herbicidal active compounds.

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The degree of identity of the amino acid sequences is determined for example with the aid of the program BLASTP + BEAUTY Version 2.0 4. (Altschul et al., 1997).

15

Preferred polypeptides which are used in the methods for finding modulators of the polypeptides according to the invention are those of SEQ ID NO: 1 to SEQ ID NO: 3227.

Based on the genetic code, a nucleic acid sequence encoding these polypeptides can be deduced in a simple fashion from the amino acid sequences of the polypeptides according to the invention, which amino acid sequences are shown in the sequence listing.

20

Such deduced nucleic acids can be used as probes and/or primers for detection and/or isolation of related polynucleotide sequences in different organisms, preferably in plants, through hybridization. Depending on the stringency of the conditions under which these probes and primers are used, polynucleotides exhibiting a wide range of similarity to those shown in Table 1 can be detected or isolated. "Stringency" as used herein is a function of probe length, probe composition (G/C content) and salt

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concentration, organic solvent concentration and temperature of hybridization or wash conditions. Stringency is typically compared by the parameter T_m , which is the temperature of hybridization or wash conditions. Stringency is typically compared by the parameter T_m which is the temperature at which 50% of the complementary molecules in the hybridization are hybridized. High stringency conditions are e.g. those providing a condition of T_m 5°C to 10°C. Medium or moderate stringency conditions are those providing T_m 20°C to t_m 29°C. Low stringency conditions are those providing for a condition of t_m 40°C to T_m 48°C. The relationship of hybridization conditions to T_m (in °C) is expressed in the following equation:

10

$$T_m = 81.5 - 16.6 (\log_{10}[\text{Na}^+] + 0.41(\%G+C)) - (600/N),$$

where N is the length of the probe. This equation works well for probes comprising 14 to 70 nucleotides in length that are identical to the target sequence.

15

Subject-matter of the present invention is therefore also the use of the nucleic acids encoding the polypeptides according to the invention in methods for finding new herbicidal compounds, and of DNA constructs which encompass one of the deduced nucleic acid sequences and a homologous or heterologous promoter.

20

The term "homologous promoter" as used in the present context refers to a promoter which controls the expression of the gene in question in the original organism.

The term "heterologous promoter" as used in the present context refers to a promoter which has properties other than the promoter which controls the expression of the gene in question in the original organism.

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The choice of heterologous promoters depends on whether pro- or eukaryotic cells or cell-free systems are used for expression. Examples of heterologous promoters are the cauliflower mosaic virus 35S promoter for plant cells, the alcohol dehydrogenase

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promoter for yeast cells, the T3, T7 or SP6 promoters for prokaryotic cells or cell-free systems.

5 Subject-matter of the present invention is furthermore vectors comprising a nucleic acid encoding a polypeptide according to the invention or an abovementioned DNA construct. Vectors which can be used are all those phages, plasmids, phagemids, phasmides, cosmids, YACs, BACs, artificial chromosomes or particles which are suitable for particle bombardment, which are used in molecular biology laboratories.

10 Preferred vectors are pBIN (Bevan, 1984) and its derivatives for plant cells, pFL61 (Minet *et al.*, 1992) or, for example, the p4XXprom. vector series (Mumberg *et al.*) for yeast cells, pSPORT vectors (Life Technologies) for bacterial cells, lambdaZAP (Stratagene) for phages or Gateway vectors (Life Technologies) for various expression systems in bacterial cells or Baculovirus.

15 Subject-matter of the present invention is furthermore host cells comprising at least one nucleic acid encoding one of the polypeptides according to the invention or a DNA construct according to the invention or a vector according to the invention.

20 The term "host cell" as used in the present context refers to cells which do not naturally comprise the nucleic acids to be used in accordance with the invention.

Suitable host cells are prokaryotic cells, preferably *E. coli*, but also eukaryotic cells, such as cells of *Saccharomyces cerevisiae*, *Pichia pastoris*, insects, plants, frog
25 oocytes and mammalian cell lines.

The term "polypeptides" as used in the present context refers not only to short amino acid chains which are usually termed peptides, oligopeptides or oligomers, but also to longer amino acid chains which are usually termed proteins. It encompasses amino
30 acid chains which can be modified either by natural processes, such as post-

translational processing, or by chemical prior-art methods. Such modifications may occur at various sites and repeatedly in a polypeptide, such as, for example, on the peptide backbone, on the amino acid side chain, on the amino and/or the carboxyl terminal. For example, they encompass acetylations, acylations, ADP ribosylations, 5 amidations, covalent linkages to flavins, haeme moieties, nucleotides or nucleotide derivatives, lipids or lipid derivatives or phosphatidylinositol, cyclisation, disulfide bridge formations, demethylations, cystine formations, formylations, gamma-carboxylations, glycosylations, hydroxylations, iodinations, methylations, myristoylations, oxidations, proteolytic processings, phosphorylations, selenoylations, 10 and tRNA-mediated amino acid additions.

The polypeptides to be used in accordance with the invention may exist in the form of "mature" proteins or as parts of larger proteins, for example as fusion proteins. They can furthermore exhibit secretion or leader sequences, pro-sequences, 15 sequences which make possible simple purification, such as polyhistidine residues, or additional stabilizing amino acids.

The polypeptides to be used in accordance with the invention need not constitute complete plant proteins but may also only be fragments thereof, as long as they retain 20 at least one biological activity of the complete plant proteins. Polypeptides which exert the same type of biological activity as one of the proteins of Table 1 are still considered as being within the scope of the present invention. In this context, it is not necessary for the polypeptides to be used in accordance with the invention to be deducible from *Arabidopsis* proteins. Polypeptides which correspond to proteins of, 25 for example, the plants given hereinbelow or fragments of these proteins which can still exert their biological activity are also considered as being within the scope of the present invention: tobacco, maize, wheat, barley, oats, oil seed rape, rice, rye, soya bean, tomatoes, legumes, potato plants, *Lactuca sativa*, Brassicae, woody species, *Physcomitrella patens*.

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In comparison with the corresponding regions of the naturally occurring polypeptides, the polypeptides according to the invention can have deletions or amino acid substitutions as long as they still exert at least one biological activity of the complete polypeptides. Conservative substitutions are preferred. Such

5 conservative substitutions encompass variations, one amino acid being replaced by another amino acid from among the following group:

1. Small aliphatic residues, unpolar residues or residues of little polarity: Ala, Ser, Thr, Pro and Gly;
- 10 2. Polar, negatively charged residues and their amides: Asp, Asn, Glu and Gln;
3. Polar, positively charged residues: His, Arg and Lys;
4. Large aliphatic unpolar residues: Met, Leu, Ile, Val and Cys; and
5. Aromatic residues: Phe, Tyr and Trp.

15 The following list shows preferred conservative substitutions:

| Original residue | Substitution |
|------------------|---------------|
| Ala | Gly, Ser |
| Arg | Lys |
| Asn | Gln, His |
| Asp | Glu |
| Cys | Ser |
| Gln | Asn |
| Glu | Asp |
| Gly | Ala, Pro |
| His | Asn, Gln |
| Ile | Leu, Val, Met |
| Leu | Ile, Val, Met |
| Lys | Arg, |
| Met | Leu, Ile |

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| Original residue | Substitution |
|------------------|-------------------------|
| Phe | Met, Leu, Tyr, Ile, Trp |
| Pro | Gly |
| Ser | Thr |
| Thr | Ser |
| Trp | Tyr, Phe |
| Tyr | Trp, Phe |
| Val | Ile, Leu |

The skilled worker knows that the polypeptides of the present invention can be obtained by various routes, for example by chemical methods such as the solid-phase method. To obtain larger protein quantities, the use of recombinant methods is recommended. The expression of a cloned gene according to the invention or fragments thereof can be effected in a series of suitable host cells which are known to the skilled worker. To this end, a nucleic acid encoding one of the polypeptides according to the invention or a DNA construct according to the invention or vector is introduced into a host cell with the aid of known methods.

10

The integration into the chromosome of the host cell, of the cloned nucleic acid according to the invention which is suitable for expressing the polypeptide according to the invention, is within the scope of the present invention. This nucleic acid or fragments thereof are preferably introduced into a plasmid, and the coding regions of the nucleic acids or fragments thereof are linked functionally to a constitutive or inducible promoter.

15

The basic steps for preparing the recombinant polypeptides according to the invention are :

20

1. Obtaining a natural, synthetic or semi-synthetic nucleic acid (DNA) which encodes a polypeptide according to the invention.

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2. Introducing this DNA into an expression vector which is suitable for expressing the polypeptide according to the invention, either alone or as a fusion protein.
 3. Transforming a suitable host cell, preferably a prokaryotic host cell, with this expression vector.
 4. Growing this transformed host cell in a manner which is suitable for expressing the polypeptide according to the invention.
 5. Harvesting the cells and isolating the polypeptide according to the invention by suitable, known methods.
- In this context, the coding regions of the polypeptide according to the invention can be expressed for example in *E. coli* using the customary methods. Suitable expression systems for *E. coli* are commercially available, for example the expression vectors of the pET series, such as pET3a, pET23a, pET28a with His-tag or pET32a with His-tag for simple purification and thioredoxin fusion for increasing the solubility of the expressed enzyme, and pGEX with glutathione synthetase fusion, and also the pSPORT vectors, with the possibility of transferring the coding region into different vectors of the Gateway system for various expression systems. The expression vectors are transformed into λ DE3-lysogenic *E. coli* strains, for example, BL21(DE3), HMS 174(DE3) or AD494(DE3). After the initial growth of the cells under standard conditions known to the skilled worker, expression is induced by means of IPTG. After induction of the cells, incubation is carried out for 3 to 24 hours at temperatures of from 18 to 37°C. The cells are disrupted by sonication in breaking buffer (10 to 200 mM sodium phosphate, 100 to 500 mM NaCl, pH 5 to 8). The protein expressed can be purified by chromatographic methods,

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in the case of protein expressed with His-tag by chromatography on an Ni-NTA column.

Another favourable approach is the expression of a polypeptide according to the invention in commercially available yeast strains (for example, *Pichia pastoris*) or in insect cell cultures (for example Sf9 cells).

Alternatively, the polypeptides according to the invention can also be expressed in plants.

A rapid method of isolating the polypeptides according to the invention which are synthesized by host cells using a nucleic acid encoding them starts with the expression of a fusion protein, it being possible for the fusion moiety to be affinity-purified in a simple manner. The fusion moiety can be, for example, glutathione S-transferase. The fusion protein can then be purified on a glutathione affinity column. The fusion moiety can be cleaved off by partial proteolytic cleavage for example at linkers between the fusion moiety and the polypeptide according to the invention which is to be purified. The linker can be designed such that it includes target amino acids, such as arginine and lysine residues, which define sites for trypsin cleavage. In order to generate such linkers, standard cloning methods using oligonucleotides may be applied.

Other purification methods which are possible are based on preparative electrophoresis, FPLC, HPLC (for example using gel filtration columns, reverse-phase columns or mildly hydrophobic columns), gel filtration, differential precipitation, ion-exchange chromatography and affinity chromatography.

The terms "isolation or purification" as used in the present context mean that the polypeptides according to the invention are separated from other proteins or other macromolecules of the cell or of the tissue. Preferably, a preparation comprising the

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polypeptides according to the invention is at least 10-fold concentrated and especially preferably at least 100-fold concentrated with regard to the protein content over a host cell preparation.

- 5 The polypeptides according to the invention can also be affinity-purified without fusion moieties with the aid of antibodies which bind to the polypeptides.

10 The polypeptides found here with the aid of the method according to the invention and the polypeptides which are homologous to them make possible the search for new specific herbicides; thus, ways are opened up of identifying lead structures, some of which may be completely new, with the aid of these targets. Thus, new interesting herbicides can be provided starting from such compounds which inhibit the present polypeptides.

- 15 Not only the enzymes, receptors and channels stated, but other proteins with other functions, too, can be filtered out for their plant specificity. This also applies to proteins whose function is as yet unknown.

20 Just as described above for finding new targets for herbicides, fungus- or insect-specific targets can be identified. For this purpose, the genomes of relevant phytopathogenic fungi, for example, *Magnaporthe* and many others, or insects, for example *Drosophila*, *Heliothis* and many others, are compared with the genomes of plants and animals. Thus, those enzymes, receptors and channels which are fungus-specific (and which do not occur in plants or animals) or which are insect-specific
25 (and which do not occur in plants or higher animals, that is to say Chordata, in particular humans), can be identified.

30 The search for lead structures by target-based screening has played a key role for approximately 10 years in the search for pharmaceutical active compounds. In crop protection research, the same key position has emerged somewhat later. Owing to

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this high relevance, a multiplicity of methods have been developed for verifying any new target. Also included are methods of expressing the genes in relevant systems with which the skilled worker in the field of various families of proteins or classes of enzymes is generally familiar.

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Enzymes and how they are affected by active compound candidate molecules can be measured quite generally on the basis of their enzymatic activity. The enzymatic conversion of starting materials to products can be determined in a multiplicity of ways: for example by monitoring the optical characteristics of the reaction solution (for example absorption, fluorescence, luminescence). If the enzymatic reaction cannot be monitored visually directly, the reaction can frequently be monitored by coupling with one or more further reactions, either enzymatic or non-enzymatic reactions, which can be monitored visually. As an alternative, a multiplicity of variants of binding assays have been developed which are based on measuring the binding of active compound candidate molecules to a protein. Binding assays can be carried out using radiolabeled or optically labeled detection molecules. Binding assays can also be carried out without labels, for example by methods of mass spectrometry or nuclear resonance spectrometry. This is in sharp contrast to the protein functions, which can be tested by cellular assays. Here, cells are constructed in a variety of ways which respond in a specific manner to the inhibition (or activation) of an enzyme (or receptor or channel). For example, bacteria can be constructed whose intrinsic enzyme has been switched off and was then replaced by a corresponding plant enzyme. When the action of active compound candidate molecules on the wild-type bacterial strain and the transgenic strain are compared, active compounds can be identified which relate to the plant enzyme. Cellular assays can preferably be used for assaying in particular receptors, but also channels. For example, non-plant cells can be constructed which recombinantly comprise a plant receptor and which visualize the response of the receptor to active compound candidate molecules visually. Thus, a luciferase can be expressed in receptor-mediated fashion, for example, and this luciferase can then be detected with high

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sensitivity. Channels which are ion-selective, in particular for calcium, can be detected for example by ion-selective stains.

5 The multiplicity of possibilities of opening up enzymes, receptors and channels to screening, preferably HTS or UHTS, is described in various reviews (see, for example, J. A. Landro et al., J. Pharmacol. Toxicol. Methods 44 (2201) 273 - 289). A large number of public fora exist for the specialists working in this field, such as, for example, the "Society for Biomolecular Screening" (Danbury, CT, USA) (www.sbsonline.org), which publishes its own periodical. The annual conferences of
10 the "Society for Biomolecular Screening" reflect the current state of the art. It can therefore be said that it is currently possible to convert any desired protein into an HTS assay, it being possible for the difficulty or complexity of the assay method to vary, depending on the polypeptide.

15 Many assay systems whose aim it is to assay compounds and natural extracts are designed for high throughput numbers in order to maximize the number of substances studied within a given period. Assay systems which are based on cell-free procedures require purified or semipurified protein. They are suitable for a "first" assay, whose principal aim is to detect a potential effect of a substance on the target
20 protein.

Effects such as cell toxicity are, as a rule, ignored in these *in vitro* systems. The assay systems test both inhibitory or suppressive effects of the substances and stimulatory effects. The efficacy of a substance can be tested by concentration-dependent test
25 series. Control batches without test substances can be used for assessing the effects.

In the following text, methods shall be shown by way of example which can be exploited inter alia for finding modulators of the polypeptides according to the invention, the methods according to the invention including high-throughput
30 screening (HTS) and ultra-high throughput screening (UHTS). Both host cells and

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cell-free preparations comprising the nucleic acids according to the invention and/or the polypeptides according to the invention can be used for this purpose.

5 The examples given are understood as being a nonlimiting selection of methods which are possible for use for the purpose in accordance with the invention.

Activity assays

10 In order to find modulators of the polypeptides to be used according to the invention, for example a synthetic reaction mix (for example products of the *in vitro* transcription) or a cellular component, such as a crude cell extract, or any other preparation comprising the polypeptide to be used in accordance with the invention can be incubated together with one or more optionally labeled substrates or ligands of the polypeptides in the presence or absence of a candidate molecule, which may be an agonist or antagonist. The ability of the candidate molecule of increasing or
15 inhibiting the activity of the polypeptide to be used in accordance with the invention can be seen from an increased or reduced conversion of the substrate. Molecules which lead to an increased activity of the polypeptides to be used in accordance with the invention are agonists. Molecules which lead to a reduction in the activity of the polypeptides to be used in accordance with the invention are probably inhibitors or
20 antagonists. The detection of the biological activity of the polypeptides to be used in accordance with the invention can possibly be improved by what is known as a reporter system. Reporter systems as used herein comprise, but are not limited to, colorimetrically labeled substrates which are converted into a product, or a reporter gene which responds to changes in the activity or the expression of the polypeptides
25 to be used in accordance with the invention.

Binding assays

30 In order to find modulators of the polypeptides to be used according to the invention, for example a synthetic reaction mix (for example products of the *in vitro* transcription) or a cellular component, such as a crude cell extract, or any other

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preparation comprising the polypeptide to be used in accordance with the invention can be incubated together with a labeled substrate or ligand of the polypeptides in the presence or absence of a candidate molecule, which may be an agonist or antagonist. The ability of the candidate molecule of increasing or inhibiting the activity of the polypeptide to be used in accordance with the invention can be seen from an increased or reduced binding of the labeled ligand. Molecules which bind well and lead to an increased activity of the polypeptides to be used in accordance with the invention are agonists. Molecules which bind well but do not trigger the biological activity of the polypeptides to be used in accordance with the invention are probably good antagonists. The detection of the biological activity of the polypeptides to be used in accordance with the invention can possibly be improved by what is known as a reporter system. Reporter systems as used herein comprise, but are not limited to, a reporter gene which responds to changes in the activity or expression of the polypeptides to be used in accordance with the invention, or other known binding assays.

Displacement assays

A further example of a method by means of which modulators of the polypeptides to be used in accordance with the invention can be found is a displacement assay in which the polypeptides to be used in accordance with the invention and a potential modulator are contacted under suitable conditions with a molecule which is known to bind to the polypeptides to be used in accordance with the invention, such as a natural substrate or ligand, or a substrate or ligand mimetic. The polypeptides to be used in accordance with the invention can be labeled themselves, for example radiolabeled or colorimetrically labeled, so that the number of the polypeptides which are bound to a ligand or which have undergone a conversion can be determined accurately. In this manner, the efficacy of an agonist or antagonist can be determined.

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For the purposes of molecular interaction studies using a polypeptide according to the invention, or else with polypeptide variants which have been modified by *in vitro* mutagenesis or other known methods, a known analytical system may be employed, for example by Biacore AB, Uppsala, Sweden. In this system, (i) the polypeptide according to the invention or fragments thereof can be coupled to a biochip via known chemical methods (coupling via amines, thiols, aldehydes) or affinity binding (for example Streptavidin-Biotin, IMAC), or (ii) a ligand, for example a peptide or a small molecule, can be coupled to the chip. The binding, to the immobilized molecules, of a ligand in solution can be measured physically. In the case of the Biocore Instrument, the ligand is immobilized on a sensor chip with a thin gold layer. The solution of the analyte is perfused through a micro-flow cell on the chip. The binding of the analyte to the immobilized ligand increases the local concentration at the surface, the refractive index of the medium close to the gold layer gradually increasing. This affects the interaction between free electrons (plasmons) in the metal and photons which are emitted by the instrument. These physical changes are proportional to the mass and molecular number on the chip, the ligand-analyte binding is registered in real time, thus allowing the apparent association/dissociation rate to be determined (Fivash et al. 1998). Competition experiments validate the specificity of the binding. Analogous measurements also serve to determine the polypeptide domains which are important for the binding of ligands, and to identify new, as yet unknown, ligands of the polypeptides according to the invention.

Scintillation Proximity Assay (SPA)

A possibility of identifying substances which modulate the activity of specific polypeptides according to the invention, such as, for example, receptor proteins, and polypeptides which are homologous thereto, is what is known as "Scintillation Proximity Assay" (SPA), see EP 015 473. This assay system exploits the interaction of a receptor with a radiolabeled ligand (for example a small organic molecule or a second radiolabeled protein molecule). The receptor is bound to microspheres or beads provided with scintillating molecules. As the radioactivity declines, the

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scintillating substance in the microsphere is excited by the subatomic particles of the radiolabel, and a detectable photon is emitted. The assay conditions are optimized in such a way that only those particles originating from the ligand lead to a signal which originate from a ligand bound to the receptor or to the polypeptide according to the invention.

In a possible embodiment, the polypeptide according to the invention is bound to the beads, either together with, or without, interacting or binding test substances. It would also be possible to use fragments of the polypeptides according to the invention. When a binding, for example radiolabeled, ligand binds to the immobilized polypeptide according to the invention, this ligand should inhibit or cancel out an existing interaction between the immobilized polypeptide according to the invention and the labeled ligand in order to bind itself in the contact area zone. Successful binding to the polypeptide according to the invention can then be detected by means of a flash of light. Analogously, an existing complex between an immobilized polypeptide and a free, labeled ligand is destroyed by the binding of a test substance, which leads to a drop in the intensity of the flash of light which is detected. In this case, the assay system corresponds to a complementary inhibition system.

20

Two Hybrid System

An example of an assay system based on intact cells is what is known as the Two Hybrid System, which is particularly suitable for those polypeptides which have a suitable interaction partner in the cell - a further polypeptide or peptide. A specific example is what is known as the interaction trap. This is a genetic selection of interacting proteins in yeast (see, for example, Gyuris *et al.* 1993). The assay system is designed to detect and describe the interaction of two proteins, owing to an interaction which has taken place leading to a detectable signal.

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Such an assay system can also be adapted to the testing of large numbers of test substances in a given period.

5 The system is based on the construction of two vectors, the bait vector and the prey vector. A gene encoding a polypeptide according to the invention or fragments thereof is cloned into the bait vector and then expressed as fusion protein together with the LexA protein, a DNA binding protein. A second gene encoding an interaction partner of the polypeptide in question is cloned into the prey vector, where it is expressed as fusion protein together with the B42 prey protein. Both
10 vectors are present in a *Saccharomyces cerevisiae* host which contains copies of LexA-binding DNA 5' of a lacZ or HIS3 reporter gene. If an interaction takes place between the two fusion proteins, activation of the transcription of the reporter gene results. If the presence of a test substance results in inhibition or interference with the interaction, the two fusion proteins can no longer interact and the product of the
15 reporter gene is no longer produced.

Calcium Imaging

Calcium imaging or signalling must be considered as a further method of detecting substances which interact with polypeptides according to the invention. This method is suitable, for example, for receptors which act as Ca^{2+} channels. Here, calcium indicators are employed with the aid of which changes in the intracellular calcium level are made detectable. Within the scope of these methods, cells which express the relevant polypeptide according to the invention are employed, and these cells are loaded with calcium indicators. Upon UV excitation, an influx of calcium caused by an HC110-R agonist, or the release of intracellular calcium, leads to a change in absorption as a function of the calcium load of the indicator. In such a system, an antagonist can be recognized by the complete or partial suppression of the calcium signal induced by the agonist (for example α -LTX). Suitable calcium indicators which are possible for this purpose are Fura-2 (Sigma) or Indo-1 (Molecular Probes).

Further calcium indicators can be excited by visible light and change their fluorescence behaviour detectably as a function of their calcium load. The indicators Fluo-3 and Fluo-4 show high affinity for calcium. Fluo-4, which has the stronger fluorescence signal, is particularly suitable for measurements in test systems where the cells are employed only at low density, as is the case for HEK293 cells. Further indicators are Rhod-2, x-Rhod-1, Fluo-5N, Fluo-5F, Mag-Fluo-4, Rhod-5F, Rhod-5N, Y-Rhod-5N, Mag-Rhod-2, Mag-X-Rhod-1, Calcium Green-1 and -2, Calcium Green-5N, Oregon Green 488 BAPTA-1, Oregon Green 488 BAPTA-2 and -5N, Fura Red, Calcein and the like.

An alternative to loading cells with calcium indicators is the recombinant expression of photoproteins in the target cells. Once these photoproteins have formed a complex with calcium ions, they react in the form of a light emission. A photoprotein which has already been used often in a large number of studies and assay systems is aequorin. In this assay method, the cells which simultaneously express the target

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protein and the aequorin are first loaded with the luminophore coelenterazin. The apoaequorin formed by the cells forms a complex with the coelenterazin and carbon dioxide. If calcium subsequently enters the cell and binds to the complex, carbon dioxide and blue light are emitted (emission maximum ~466 nm). The light emission
5 correlates with the calcium concentration which prevails intracellularly.

Subject-matter of the present invention is therefore in particular also the use of the polypeptides of the Table 1 which have been identified with the aid of the present method in methods of finding modulators of the polypeptides according to the
10 invention.

Subject-matter of the present invention is furthermore the use of nucleic acids encoding these plant proteins, DNA constructs comprising them, host cells comprising them, or antibodies which bind to these proteins in methods of finding
15 modulators of the polypeptides according to the invention.

The term "agonist" as used in the present context refers to a molecule which accelerates or increases the activity of the protein.

20 The term "antagonist" as used in the present context refers to a molecule which slows down or prevents the activity of the protein.

The term "modulator" as used in the present context constitutes the generic term for agonist and antagonist. Modulators can be small organochemical molecules, peptides
25 or antibodies which bind to the polypeptides to be used in accordance with the invention. Furthermore, modulators can be small organochemical molecules, peptides or antibodies which bind to a molecule which, in turn, binds to the polypeptides to be used in accordance with the invention, thus influencing their biological activity. Modulators can constitute natural substrates and ligands or of

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structural or functional mimetics thereof. However, the term "modulator" does not extend to the natural substrates and to ATP.

The modulators are preferably small organochemical compounds.

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The binding of the modulators to the proteins to be used in accordance with the invention can modify the cellular processes in such a way which lead to the death of the plants treated therewith.

10 Subject-matter of the present invention are therefore also modulators which have been found with the aid of one of the polypeptides described in accordance with SEQ ID NO:1 to SEQ ID NO:3227 for identifying modulators of a polypeptide.

15 Subject-matter of the invention is furthermore the use of modulators of the polypeptides in accordance with SEQ ID NO:1 to SEQ ID NO:3227 as herbicides.

Furthermore, the present invention comprises methods of finding chemical compounds which modify the expression of the polypeptides to be used in accordance with the invention. Such "expression modulators", again, can constitute
20 growth-regulatory or herbicidal active compounds. Expression modulators can be small organochemical molecules, peptides or antibodies which bind to the regulatory regions of the nucleic acids encoding the polypeptides which are to be used in accordance with the invention. Furthermore, expression modulators can be small organochemical molecules, peptides or antibodies which bind to a molecule which,
25 in turn, binds to regulatory regions of the nucleic acids encoding the polypeptides to be used in accordance with the invention, thus influencing their expression. Expression modulators can also be antisense molecules.

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The present invention therefore also extends to the use of modulators of the polypeptides according to the invention or of expression modulators of same as plant growth regulators or herbicides.

5 Subject-matter of the present invention are also expression modulators of proteins which are found with the aid of any above-described method of identifying expression modulators of the proteins.

10 Subject-matter of the invention is also the use of expression modulators as herbicides.

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Patent Claims

1. Method of identifying target proteins for herbicidally active compounds,
comprising the following steps:
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a) alignment of a nucleic acid sequence or amino acid sequence (Group 1
sequence) from plants with a nucleic acid sequence or amino acid
sequence from non-plant organisms (group 2 sequence) using suitable
search parameters,
10
b) determination of the E-value of the group 1 sequence and a similar
group 2 sequence, and
c) selecting group 1 sequences in which the exponent of the E-value
15 exceeds that of the most similar group 2 sequence at least by a factor
of 3.
2. Method according to Claim 1, characterized in that, in a further step, those
group 1 sequences are selected which are essential for the plant and, if
20 appropriate, naturally have small ligands.
3. Method according to Claim 1 or 2, characterized in that the E-value is not
lower than 10^{-30} .
25 4. Use of polypeptides or of nucleic acids encoding them which are found in a
method according to one of Claims 1 to 3 in a method of identifying
modulators of these polypeptides or nucleic acids.

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5. Use of one of the polypeptides in accordance with SEQ ID NO: 1 to SEQ ID NO: 3227 and of the nucleic acids encoding them in methods of identifying modulators of these polypeptides.
- 5 6. Method of finding a chemical compound which modulates the activity of one of the polypeptides in accordance with SEQ ID NO: 1 to SEQ ID NO: 3227, comprising the following steps:
 - 10 (a) contacting a preparation or host cell comprising the polypeptide with a chemical compound or a mixture of chemical compounds under conditions which permit the interaction of a chemical compound with the polypeptide, and
 - 15 (b) identifying the chemical compound which specifically influences the activity of the polypeptide.
7. Method of finding a chemical compound which binds to one of the polypeptides in accordance with SEQ ID NO: 1 to SEQ ID NO: 3227 and/or which displaces a natural substrate or a natural ligand, comprising the following steps:
 - 20 (a) contacting a preparation or host cell comprising the polypeptide with a chemical compound or a mixture of chemical compounds under conditions which permit the interaction of a chemical compound with the polypeptide, and
 - 25 (b) identifying the chemical compound which specifically binds to the polypeptide, and/or

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- (c) identifying the chemical compound which specifically displaces a natural substrate or a natural ligand.
- 5 8. Method of finding a chemical compound which modulates the cellular function of one of the polypeptides in accordance with SEQ ID NO: 1 to SEQ ID NO: 3227, comprising the following steps:
- 10 (a) contacting a host cell which expresses the polypeptide with a chemical compound or a mixture of chemical compounds under conditions which permit the interaction of the chemical compound with the cell and/or the polypeptide, and
- 15 (b) identifying the chemical compound which specifically influences the cellular function of the polypeptide.
9. Method of finding a compound which modifies the expression of the polypeptide in accordance with SEQ ID NO: 1 to SEQ ID NO: 3227, comprising the following steps:
- 20 (a) contacting a host cell expressing the polypeptide with a chemical compound or a mixture of chemical compounds,
- (b) determining the polypeptide concentration, and
- 25 (c) identifying the compound which specifically influences the expression of the polypeptide.
10. Use of a modulator of one of the polypeptides in accordance with SEQ ID NO: 1 to SEQ ID NO: 3227 as herbicide.

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11. Herbicides which are found in a method according to Claim 6 or 7.